The Mapping of Chromosome 16

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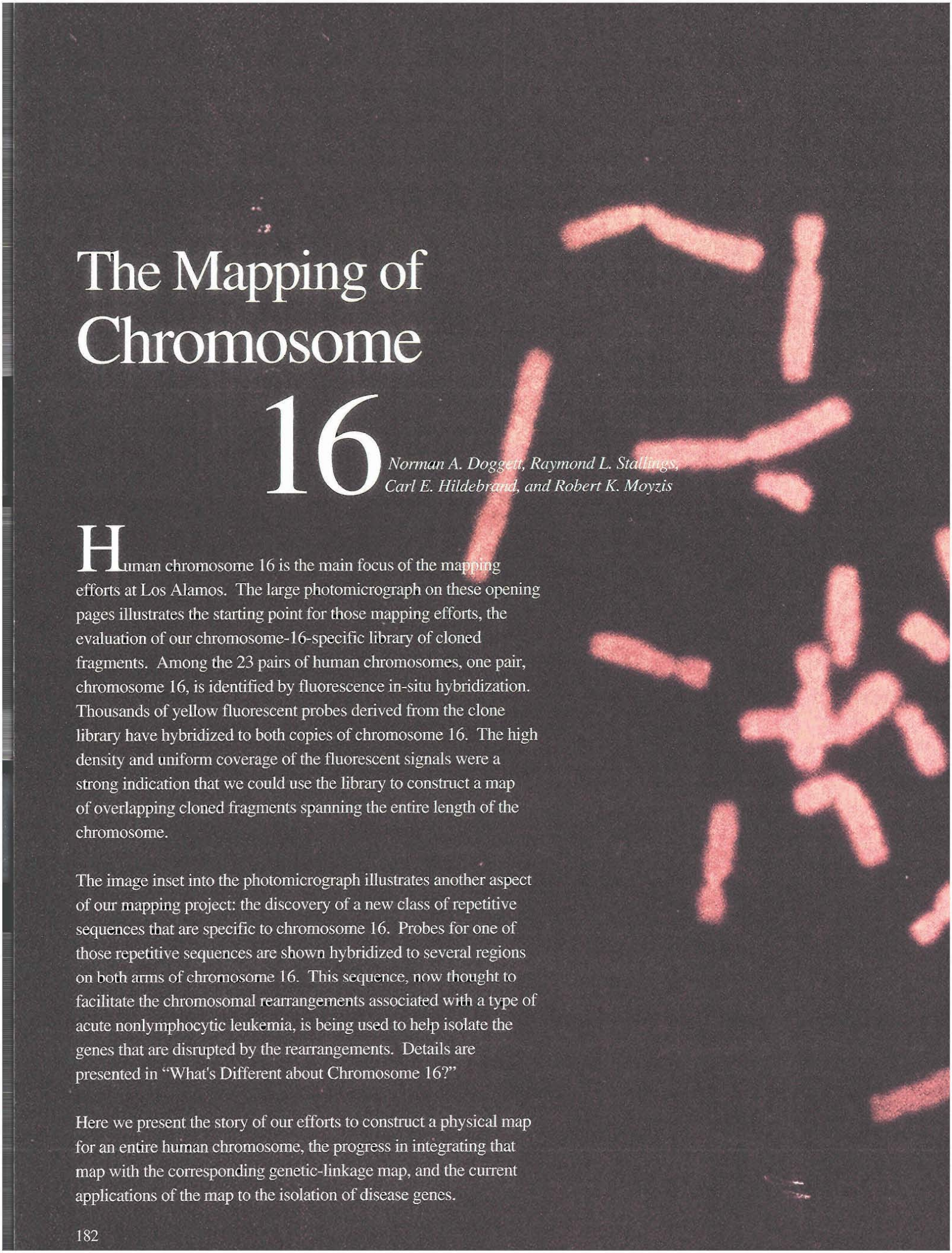
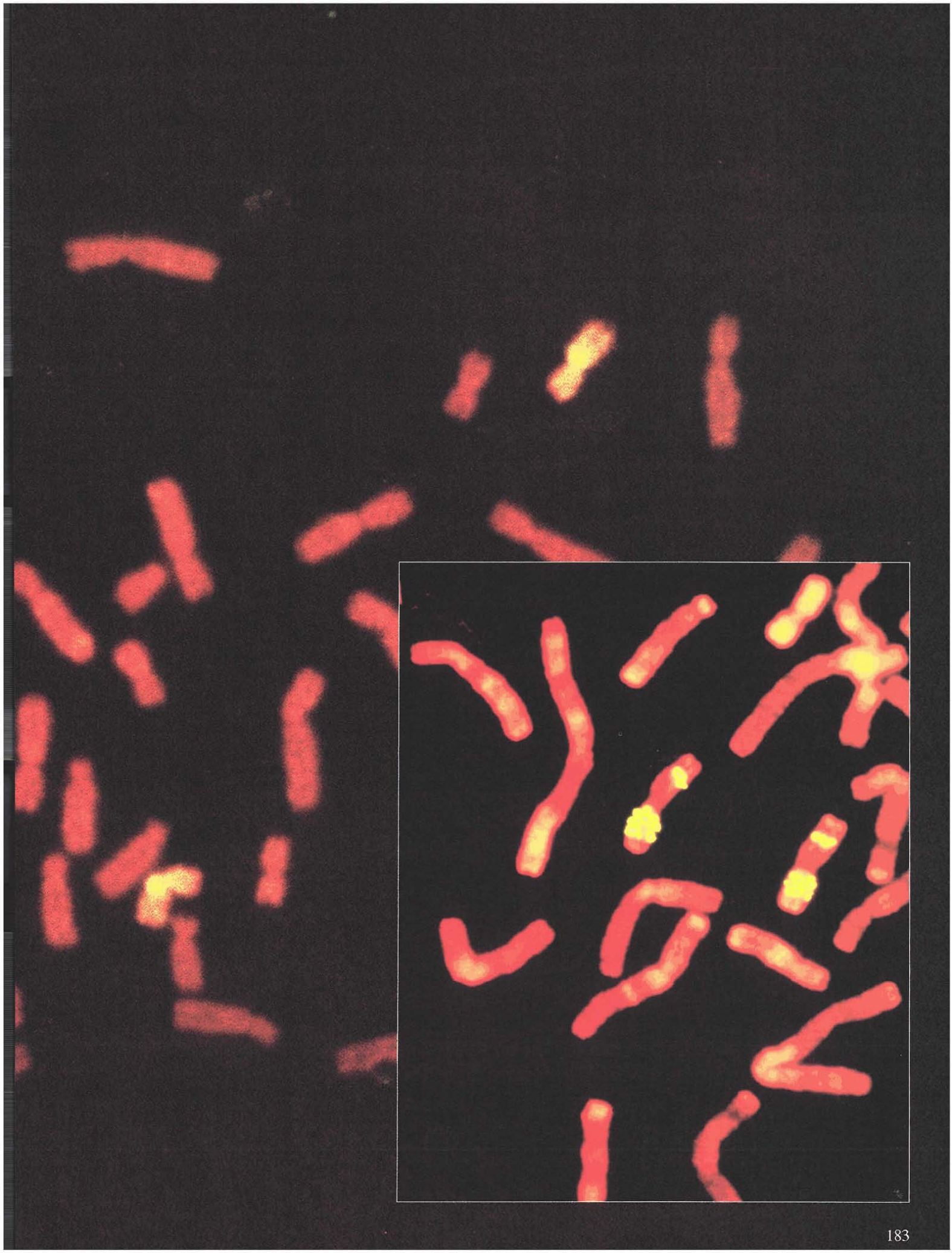


Human chromosome 16 is the main focus of the mapping efforts at Los Alamos. The large photomicrograph on these opening pages illustrates the starting point for those mapping efforts, the evaluation of our chromosome-16-specific library of cloned fragments. Among the 23 pairs of human chromosomes, one pair, chromosome 16, is identified by fluorescence in-situ hybridization. Thousands of yellow fluorescent probes derived from the clone library have hybridized to both copies of chromosome 16. The high density and uniform coverage of the fluorescent signals were a strong indication that we could use the library to construct a map of overlapping cloned fragments spanning the entire length of the chromosome.

The image inset into the photomicrograph illustrates another aspect of our mapping project: the discovery of a new class of repetitive sequences that are specific to chromosome 16. Probes for one of those repetitive sequences are shown hybridized to several regions on both arms of chromosome 16. This sequence, now thought to facilitate the chromosomal rearrangements associated with a type of acute nonlymphocytic leukemia, is being used to help isolate the genes that are disrupted by the rearrangements. Details are presented in "What's Different about Chromosome 16?"

Here we present the story of our efforts to construct a physical map for an entire human chromosome, the progress in integrating that map with the corresponding genetic-linkage map, and the current applications of the map to the isolation of disease genes.



Setting the Stage

Both the molecular and the physical technology for constructing physical maps of complex genomes have developed at a blistering pace over the past five years, due largely to the initiation of the Human Genome Project. These technologies include the cloning of very large DNA fragments, electrophoretic separation of million-base-sized DNA fragments, and sequence-based mapping using the polymerase chain reaction (PCR) to identify unique sequences along the genome. The latter provides a language for interrelating various types of genome maps. The significance of these developments is discussed in Part II of "Mapping the Genome."

In 1988, when our laboratory initiated the physical mapping of chromosome 16, the cloning of very large DNA fragments in yeast artificial chromosomes (YACs) was just beginning in a handful of laboratories and only one library of YAC clones containing all the DNA in the human genome had been constructed worldwide. The total human-genomic YAC library was constructed at Washington University, where the technique of YAC cloning had originally been developed. The polymerase chain reaction had not yet become a standard tool of molecular biology, and the use of sequence-tagged sites (STSs) as unique DNA landmarks for physical mapping had not yet been conceived (see "The Polymerase Chain Reaction and Sequence-tagged Sites" in "Mapping the Genome"). Thus, in 1988 the most modern tools for large-scale physical mapping of human chromosomes were still waiting in the wings. On the other hand, a number of mapping techniques had been developed and were being applied to the genomes of some of the favorite organisms of molecular biologists.

Cassandra Smith and Charles Cantor had used pulsed-field gel electrophoresis to order the very large restriction fragments produced by cutting the *E. coli* genome with two rare-cutting restriction enzymes. The resulting long-range restriction map of *E. coli* demonstrated that pulsed-field gel electrophoresis is a way to study the long-range order of landmarks on the DNA of human chromosomes. Contig maps, or physical maps of ordered, overlapping cloned fragments, were near completion for the genomes of *E. coli* (about 5 million base pairs) and the yeast *S. cerevisiae* (about 13 million base pairs). Those maps were constructed using lambda-phage clones, which carry an average DNA insert size of 20,000 base pairs. Work had also begun on mapping the genome of the nematode (100 million base pairs) using cosmid clones. Cosmids carry the much longer average insert size of 35,000 base pairs.

The haploid human genome, which includes one copy of each human chromosome, has 3 billion base pairs and is therefore about 250 times the size of the yeast genome and 30 times the size of the nematode genome. When plans for the Human Genome Project were being discussed in the late 1980s, it was natural to consider dividing the human genome by chromosome and mapping one chromosome at a time.

Ongoing work at Los Alamos on human DNA and on adapting flow-sorting technology to separating individual human chromosomes set the stage for the Laboratory to play a key role in the Human Genome Project. In particular, as part of the National Gene Library Project, a group led by Larry Deaven had constructed twenty-four libraries, or unordered collections of lambda-phage clones, each containing DNA from one of the twenty-four human chromosomes (see "Libraries from Flow-sorted Chromosomes"). Those chromosome-specific libraries were designed as a source of probes to find polymorphic DNA markers for constructing genetic-linkage maps (see "Modern Linkage Mapping") and as a source of clones for rapid isolation of genes using cDNAs, or coding-region probes, to pick out the appropriate clones from the libraries. Deaven and his group were also constructing larger-insert chromosome-specific libraries using cosmid vectors. The large DNA inserts were prepared by partially digesting sorted chromosomes with restriction enzymes, thereby creating overlapping fragments. The cloned fragments would therefore be useful in constructing physical maps of ordered, overlapping clones covering extended regions of human chromosomes. Among the first chromosome-specific cosmid libraries to be constructed at Los Alamos was one for human chromosome 16.

Human chromosomes range in size from 50 million base pairs for chromosome 21 to 263 million base pairs for chromosome 1. Chromosome 16, which is about 100 million base pairs in length, was chosen as our primary target for large-scale physical mapping. We selected chromosome 16 for a number of technical reasons including: (1) the availability of a hybrid-cell line containing a single copy of chromosome 16 in a mouse-chromosome background, which permitted accurate sorting of human chromosome 16 from the mouse chromosomes and thus the construction of a high-purity chromosome 16-specific library of cosmid clones for use in map construction; (2) identification of a chromosome 16-specific satellite repetitive-sequence probe permitting accurate purity assessments of sorted chromosomes; and (3) the availability,

[***Opening pages: large photomicrograph courtesy of Evelyn Campbell; inset image courtesy of David Ward, Yale University School of Medicine.***]

Table 1. Disease Genes Localized to Human Chromosome 16

Location	Symbol	Cloned	Disease
16p13.3	HBA	Yes	Thalassemia
16p13.3	PKD1	No	Autosomal dominant polycystic kidney disease
16p13.3	MEF	No	Familial Mediterranean fever
16p13.3	RTS	No	Rubinstein-Taybi syndrome
16p12	CLN3	No	Batten's disease (juvenile-onset neuronal ceroid lipofuscionosis)
16q12	PHKB	No	Glycogen-storage disease, type VIIIb
16q13	CETP	Yes	Elevated high-density lipoprotein (HDL), (CETP deficiency)
16q22.1	LCAT	Yes	Corneal opacities, anemia, proteinuria with unesterified hypercholesterolemia (Norum disease)
16q22.1	TAT	Yes	Richner-Hanhort syndrome, oculocutaneous tyrosinemia II (TAT deficiency)
16q22.1	ALDOA	Yes	Hemolytic anemia (ALDOA deficiency)
16q24.3	APRT	Yes	Urolithiasis, 2,5 dihydroxyadenine (APRT) deficiency
16q24	CYBA	No	Autosomal chronic granulomatous disease
16q	CTM	No	Marner's cataract
16q	CMH2	No	Familial hypertrophic cardiomyopathy

through collaboration, of a panel of a large number of hybrid-cell lines containing portions of chromosome 16. This hybrid-cell panel enables probes from chromosome 16 to be localized into intervals along the chromosome having an average length of 1.6 million base pairs.

Chromosome 16 is also interesting to the biomedical community. It contains gene loci for several human diseases of both clinical and economic importance, including polycystic kidney disease, a class of hemoglobin disorders, and several types of cancer (including leukemia and breast cancer). Table 1 lists disease genes that have been localized to chromosome 16 through genetic-linkage analysis. A physical map of overlapping clones for chromosome 16 would facilitate rapid isolation of those genes not yet cloned.

It takes about 2500 cosmid clones laid end to end to represent all the DNA in chromosome 16 once, and so our chromosome 16-specific library of 25,000 cosmid clones represented a tenfold coverage of the chromosome. In 1988, with funds from the Department of Energy, we took on the physical mapping of chromosome 16.

Developing a Mapping Strategy

Our initial strategy for constructing an ordered-clone, or contig, map for chromosome 16 was to fingerprint cosmid clones chosen at random, determine the overlaps between pairs of clones from the similarities between fingerprints, and assemble the clone pairs into contigs, or islands of overlapping clones. This basic clone-to-fingerprint-to-contig strategy, which is described in "Physical Mapping—A One-Dimensional Jigsaw Puzzle" in "Mapping the Genome", had been applied successfully to the mapping of the *E. coli*, yeast, and nematode genomes. However, those maps of less complex genomes had taken many years of work. In addition, the human genome contains many classes of repetitive sequences that tend to complicate the process of building contigs. When faced with the mapping of human chromosome 16, which is about ten times larger than

the yeast genome, we needed to develop a strategy that would increase the speed of contig building while retaining the required accuracy.

Lander and Waterman's 1988 analysis of random-clone fingerprinting suggested the key to increased mapping efficiency. That paper showed that the size of the smallest detectable clone overlap was an important parameter in determining the rate at which contigs would increase in length and therefore the rate at which contig maps would near completion. In particular, the calculated rate of progress increases significantly if the detectable clone overlap is reduced from 50 percent to 25 percent of the clone lengths.

In the mapping efforts for yeast and *E. coli*, the overlap between two clones was detected by preparing a restriction-fragment fingerprint of each clone and identifying restriction-fragment lengths that were common to the two fingerprints. With this method, two clones have to overlap by at least 50 percent in order for one to declare with a high degree of certainty that the two clones do indeed overlap. (See "Physical Mapping—A One-Dimensional Jigsaw Puzzle" for a description of restriction-fragment fingerprinting.) Clearly, increasing the information content in each clone fingerprint would make smaller overlaps detectable.

The Repetitive-Sequence Fingerprint

The unique feature of our initial mapping strategy was what we call the repetitive-sequence fingerprint. Repetitive sequences compose 25 to 35 percent of the human genome. The box at right shows the most abundant classes of repetitive sequences and the approximate locations of those sequences on human chromosome 16.

Various Classes of Human Repetitive DNA Sequences

Described below are the most abundant classes of repetitive DNA on human chromosomes. The figure shows the locations of these classes on chromosome 16. Numbers in parentheses indicate the size of continuous stretches of each repetitive DNA class.

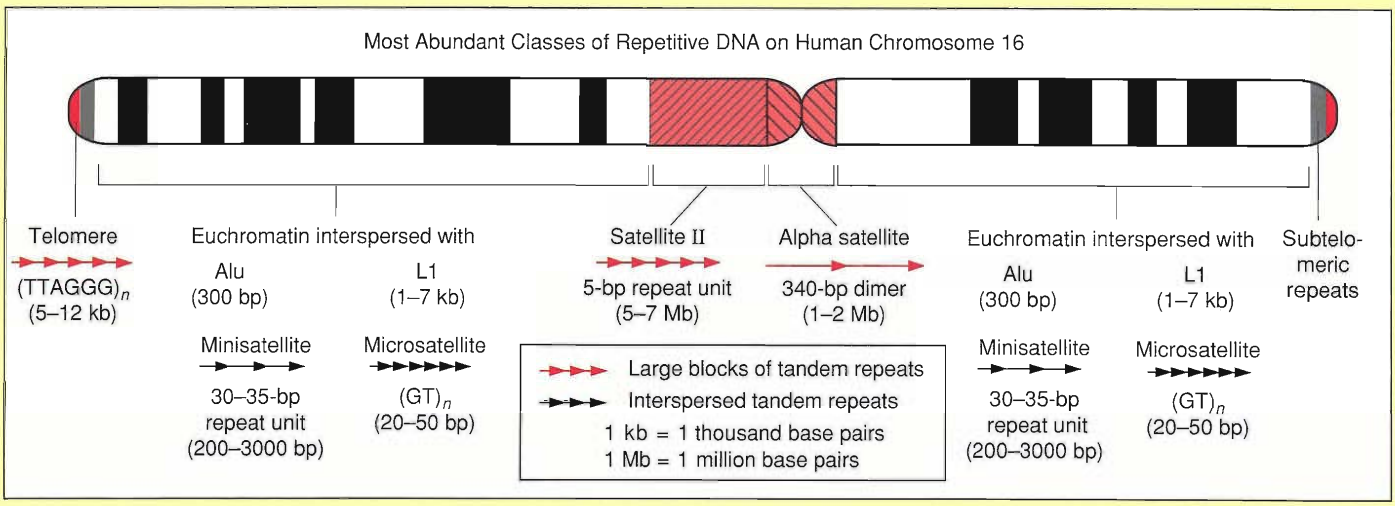
Telomere Repeat: The tandemly repeating unit TTAGGG located at the very ends of the linear DNA molecules in human and vertebrate chromosomes. The telomere repeat $(TTAGGG)_n$ extends for 5000 to 12,000 base pairs and has a structure different from that of normal DNA. A special enzyme called telomerase replicates the ends of the chromosomes in an unusual fashion that prevents the chromosome from shortening during replication.

Subtelomeric repeats: Classes of repetitive sequences that are interspersed in the last 500,000 bases of nonrepetitive DNA located adjacent to the telomere. Some sequences are chromosome specific and others seem to be present near the ends of all human chromosomes.

Microsatellite repeats: A variety of simple di-, tri-, tetra-, and penta-nucleotide tandem repeats that are dispersed in the euchromatic arms of most chromosomes. The dinucleotide repeat $(GT)_n$ is the most common of these dispersed repeats, occurring on average every 30,000 bases in the human genome, for a total copy number of 100,000. The GT repeats range in size from about 20 to 60 base pairs and appear in most eukaryotic genomes.

Minisatellite repeats: A class of dispersed tandem repeats in which the repeating unit is 30 to 35 base pairs in length and has a variable sequence but contains a core sequence 10 to 15 base pairs in length. Minisatellite repeats range in size from 200 base pairs up to several thousand base pairs, have lower copy numbers than microsatellite repeats, and tend to occur in greater numbers toward the telomeric ends of chromosomes.

Alu repeats: The most abundant interspersed repeat in the human genome. The Alu sequence is 300 base pairs long and occurs on average once every 3300 base pairs in the human genome, for a total copy number of 1 million. Alus are more abundant in the light bands than in the dark bands of giemsa-stained metaphase chromosomes. They occur throughout the primate family and are homologous to and thought to be descended from a small, abundant RNA gene that codes for the 300-nucleotide-long RNA molecule known as 7SL. The 7SL RNA combines with six proteins to form a protein-RNA complex that recognizes the signal sequences of newly synthesized proteins and aids in their translocation through the membranes of the endoplasmic recticulum (where they are formed) to their ultimate destination in the cell.



L1 repeats: A long interspersed repeat whose sequence is 1000 to 7000 base pairs long. L1s have a common sequence at the 3′ end but are variably shortened at the 5′ end and thus have a large range of sizes. They occur on average every 28,000 base pairs in the human genome, for a total copy number of about 100,000, and are more abundant in Giemsa-stained dark bands. L1 repeats are also found in most other mammalian species. Full-length L1s (3.5 percent of the total) are a divergent group of class II retrotransposons—"jumping genes" that can move around the genome and are thought to be remnants of retroviruses. [Class II retrotransposons have at least one protein-coding gene and contain a poly A tail (or series of As at the 3′ end) as do messenger RNAs.] Recently, a full-length, functional L1 was discovered. It was found to code for a functional reverse transcriptase—an enzyme essential to the process by which the L1s are copied and re-inserted into the genome.

Alpha satellite DNA: A family of related repeats that occur as long tandem arrays at the centromeric region of all human chromosomes. The repeat unit is about 340 base pairs and is a dimer, that is, it consists of two subunits, each about 170 base pairs long. Alpha satellite DNA occurs on both sides of the centromeric constriction and extends over a region 1000 to 5000 base pairs long. Alpha satellite DNA in other primates is similar to that in humans.

Satellite I, II, and III repeats: Three classical human satellite DNAs, which can be isolated from the bulk of genomic DNA by centrifugation in buoyant density gradients because their densities differ from the densities of other DNA sequences. Satellite I is rich in As and Ts and is composed of alternating arrays of a 17- and 25-base-pair repeating unit. Satellites II and III are both derived from the simple five-base repeating unit ATTCC. Satellite II is more highly diverged from the basic repeating unit than Satellite III. Satellites I, II and III occur as long tandem arrays in the heterochromatic regions of chromosomes 1, 9, 16, 17, and Y and the satellite regions on the short (p) arms of chromosomes 13, 14, 15, 21, and 22.

Cot1 DNA: The fraction of repetitive DNA that is separable from other genomic DNA because of its faster re-annealing, or renaturation, kinetics. *Cot* 1 DNA contains sequences that have copy numbers of 10,000 or greater. ■

Our work on the distribution of repetitive sequences had shown that the tandem-repeat sequence $(GT)_n$, where n is typically between 15 and 30, was scattered randomly across most regions of the human genome with an average spacing of 30,000 base pairs. The in-situ hybridization in Figure 1 shows that $(GT)_n$ is scattered throughout the arms of human chromosomes but is noticeably absent from the regions around the centromere. (The centromeric regions consists of large blocks of tandem-repeat sequences known as satellite DNA. Gene sequences are absent from these regions. Regions containing large blocks of tandem repeats are known as heterochromatin, and regions devoid of large tandem repeat blocks are known as euchromatin.)

We reasoned that the sequence $(GT)_n$ would appear, on average, about once in each cosmid clone containing a human DNA insert of 35,000 base pairs from the euchromatic arms of chromosome 16. Therefore, we could enrich the information content of the usual restriction-fragment fingerprint of each clone by determining, through hybridization of a radio-labeled $(GT)_{25}$ probe, which restriction fragments in each fingerprint contain the $(GT)_n$ sequence. As we will illustrate below, this information allowed us to detect overlaps between cosmid clones that were as small as 10 percent of their lengths.

To reduce the initial complexity of the mapping, we preselected from our chromosome 16-specific library of clones (through hybridization) those clones that were positive for the $(GT)_n$ sequence and negative for satellite DNA. In other words, we chose to build contigs around those sites in chromosome 16 that contain $(GT)_n$. Since those sites are widely scattered across the chromosome, we expected those contigs to cover the chromosome in a fairly uniform way except for the centromeric region, which can be mapped using an alternative approach. We identified about 3000 $(GT)_n$-positive clones from our library and made a repetitive-sequence fingerprint for each one.

Figure 1. GT Hybridization on Human Chromosomes

The photomicrograph shows in-situ hybridization of human chromosomes using biotin-labeled $(AC)_{25}$ as a probe (yellow). $(AC)_{25}$ hybridizes to sites of the microsatellite repeat $(GT)_n$. Those sites are underrepresented at the centromeric regions of some chromosomes and at the distal half of Yq. However, $(GT)_n$ appears to be uniformly distributed on all euchromatic regions of the human genome.

The repetitive-sequence fingerprint was made by digesting each cosmid clone with restriction enzymes, sizing the resulting restriction fragments, and determining which of those fragments contain $(GT)_n$ as well as another type of repetitive DNA known as *Cot*1, which is also scattered throughout the arms of the chromosome (see box). *Cot*1 is the most abundant fraction of repeated DNA in the human genome, consisting predominantly of Alu and L1 repeated sequences.

The first step in fingerprinting was to isolate many copies of the DNA insert in each cosmid clone, divide those copies into three batches, and digest each batch with the restriction enzymes *Eco*RI, *Hin*dIII, and a mixture of both *Eco*RI and *Hin*dIII, respectively. The restriction fragments from each of the three digests were separated in parallel along three lanes of an agarose gel by electrophoresis. DNA fragments having known lengths were separated on adjacent lanes to determine the fragment lengths from each restriction-enzyme digest. The fragments in the gel were stained with ethidium bromide (a fluorescent dye that binds to DNA) and the gel was photographed under ultraviolet light to produce an image

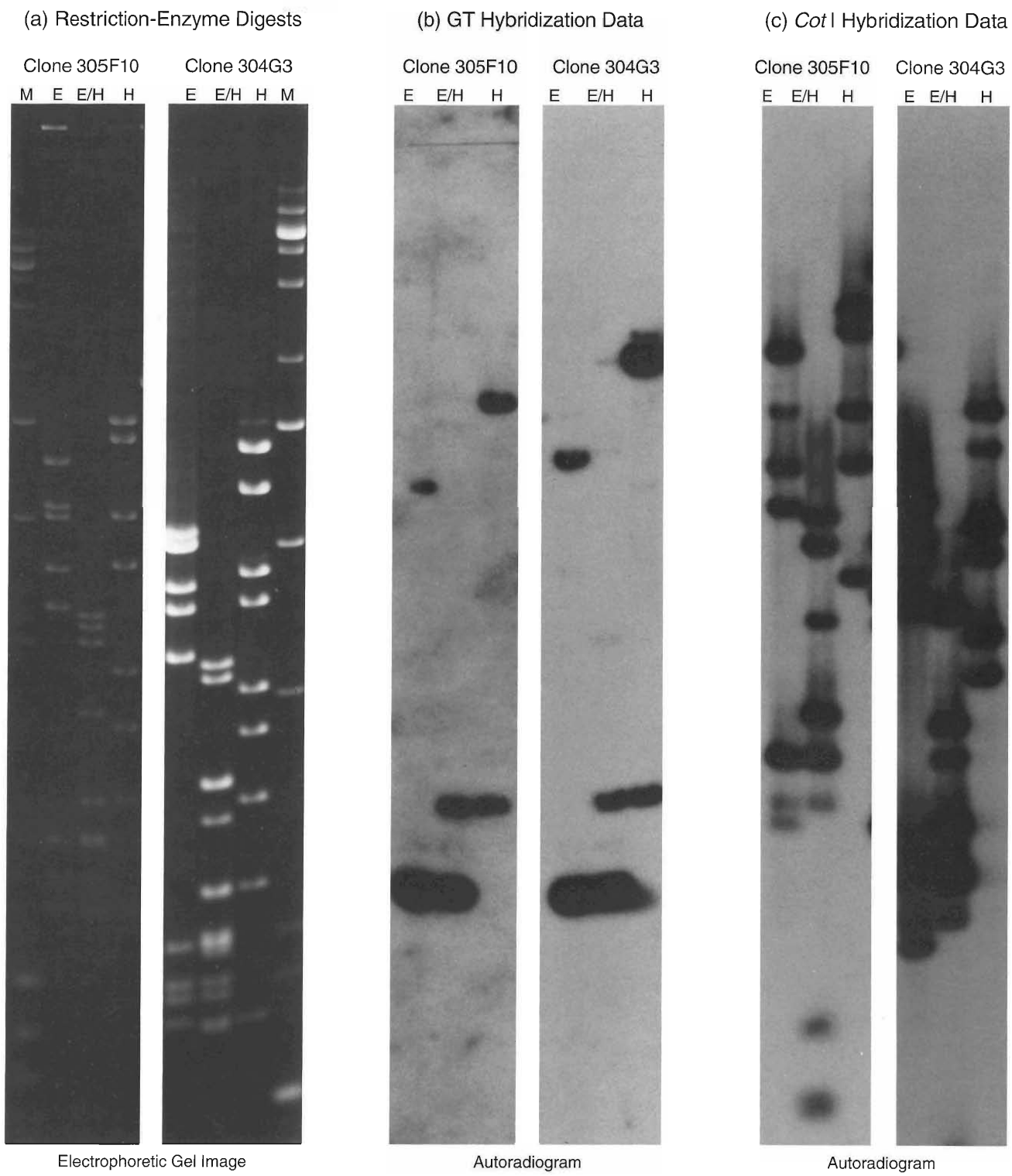


Figure 2. Repetitive Sequence Fingerprints of Two Overlapping Cosmid Clones

The repetitive-sequence fingerprint of a clone has three parts. The figure shows a comparison of those parts for two clones that have a high likelihood of overlap based on the similarities between their fingerprints. (a) Fluorescent images of DNA fragments separated by agarose gel electrophoresis. The three gel lanes for each clone contain the restriction fragments produced by completely digesting that clone with the restriction enzymes *Eco*RI (E), *Eco*RI and *Hind* III (E/H), and *Hind* III (H), respectively. The marker lanes (M) contain standard fragments of known lengths, which are used to calibrate the restriction-fragment lengths. (b) Autoradiographic images of the gels in (a) after hybridization with the GT probe. (c) Autoradiographic images of the gels in (a) after hybridization with the *Cot*1 probe. Clone 305F10 and clone 304G3 have identical GT-hybridization patterns, a strong indication of overlap.

showing the distinct bands of DNA fragments in the gel, each band made up of many copies of a particular restriction fragment. This gel image was then digitized with a CCD camera, the DNA fragments were assigned sizes according to their positions on the gel relative to the known fragment lengths using a commercial software package. These sizes were the stored in our mapping database. Figure 2 shows the gel images for two clones that were determined to overlap one another based on their complete repetitive-sequence fingerprints.

The second step in fingerprinting was to determine which restriction fragments contained $(GT)_n$ and *Cot*1 repetitive DNA. We accomplished this step using standard hybridization techniques. (See "Hybridization Techniques" in "Understanding Inheritance.") Specifically, DNA from each gel was transferred to two different nylon or nitrocellulose membranes using the blotting procedure developed by Edwin Southern in 1975. This blotting procedure preserves the relative positions that the DNA fragments have on the gel. Once the fragments are immobilized on the two membranes, radio-labeled copies of the $(GT)_n$ sequence are used as hybridization probes on one membrane and radio-labeled copies of the *Cot*1 sequences are used as probes on the second membrane. The bands of fragments that contain those sequences and therefore bind, or hybridize, to the radioactive probes can be visualized by exposing an x-ray film to the membrane, a process known as autoradiography. Alongside the gel images shown in Figure 2 are the corresponding autoradiographs, or blot images, produced by the $(GT)_n$ hybridization and *Cot*1 hybridization. Together, the gel image and the two blot images for each clone constitute the repetitive-sequence fingerprint of that clone.

The fingerprint data are scored by first noting the lengths of the restriction fragments on the gel image. Then the gel image and the two blot images for each clone are aligned to determine the hybridization score of each band of restriction fragments. To help us accomplish this task for thousands of clones in an efficient manner, Mike Cannon of the Computer Division at Los Alamos developed a computer program called SCORE. This program takes the fragment lengths determined from the gel image and creates a schematic of the gel image. The blot image is then scanned, and its image size is adjusted to match the schematic of the gel image. Each band is then scored for the presence or absence of a positive hybridization signal from the $(GT)_n$ probe and for the degree of hybridization of the *Cot*1 probe. *Cot*1 creates a low, medium, or high hybridization signal depending on whether the restriction fragment contains short, intermediate, or long stretches of *Cot*1 sequences. (Operation of the SCORE program is illustrated in "SCORE: A Program for Computer-assisted Scoring of Southern Blots" in "Computation and the Human Genome Project.")

Determining the Likelihood That Two Clones Overlap

Once the clones have been fingerprinted and the fingerprint data scored and entered into the database, the next step is to determine from the similarities between fingerprints which pairs of clones overlap one another. The problem of determining clone overlap from such fingerprint data is probabilistic, as explained in "Physical Mapping—A One-Dimensional Jigsaw Puzzle." We have two types of information, the sizes of the restriction fragments and the hybridization scores for each fragment. The two questions we need to answer are: Given that the fingerprints of two clones share certain restriction-fragment lengths and hybridization scores, first, what is the probability that they overlap? and second, what is the extent of that overlap?

The first question was addressed by David Torney, a member of the Theoretical Biology and Biophysics Group at Los Alamos. He and his collaborator David Balding developed a complete statistical analysis of the problem, taking into account the known statistical properties of the restriction-fragment lengths, experimental errors in restriction-fragment lengths, hybridization errors, and the expected distribution of the repetitive sequences. They also developed a simplified computer algorithm based on their complete theoretical analysis and on extensive analysis of the actual fingerprint data generated at Los Alamos. That algorithm determines the likelihood that two cosmid clones overlap given the repetitive-sequence fingerprints of those clones.

Figure 3 illustrates how the information content in the repetitive-sequence fingerprint allows the detection of small overlaps. In particular, when $(GT)_n$ is present in the overlap region of two clones, the similarities between the repetitive-sequence fingerprints of those clones yield a nearly unambiguous signature of overlap, even if the region of overlap is small. In the example shown, clones A and B have only a 10 percent overlap, but the overlap region contains the single $(GT)_n$ sequence present on those clones along with two cutting sites for *Eco*RI and one cutting site for *Hin*dIII. Consequently the GT hybridization patterns on the blot images of the two clones are identical within experimental errors and contain one GT-positive band for each restriction-enzyme digest. The likelihood that two

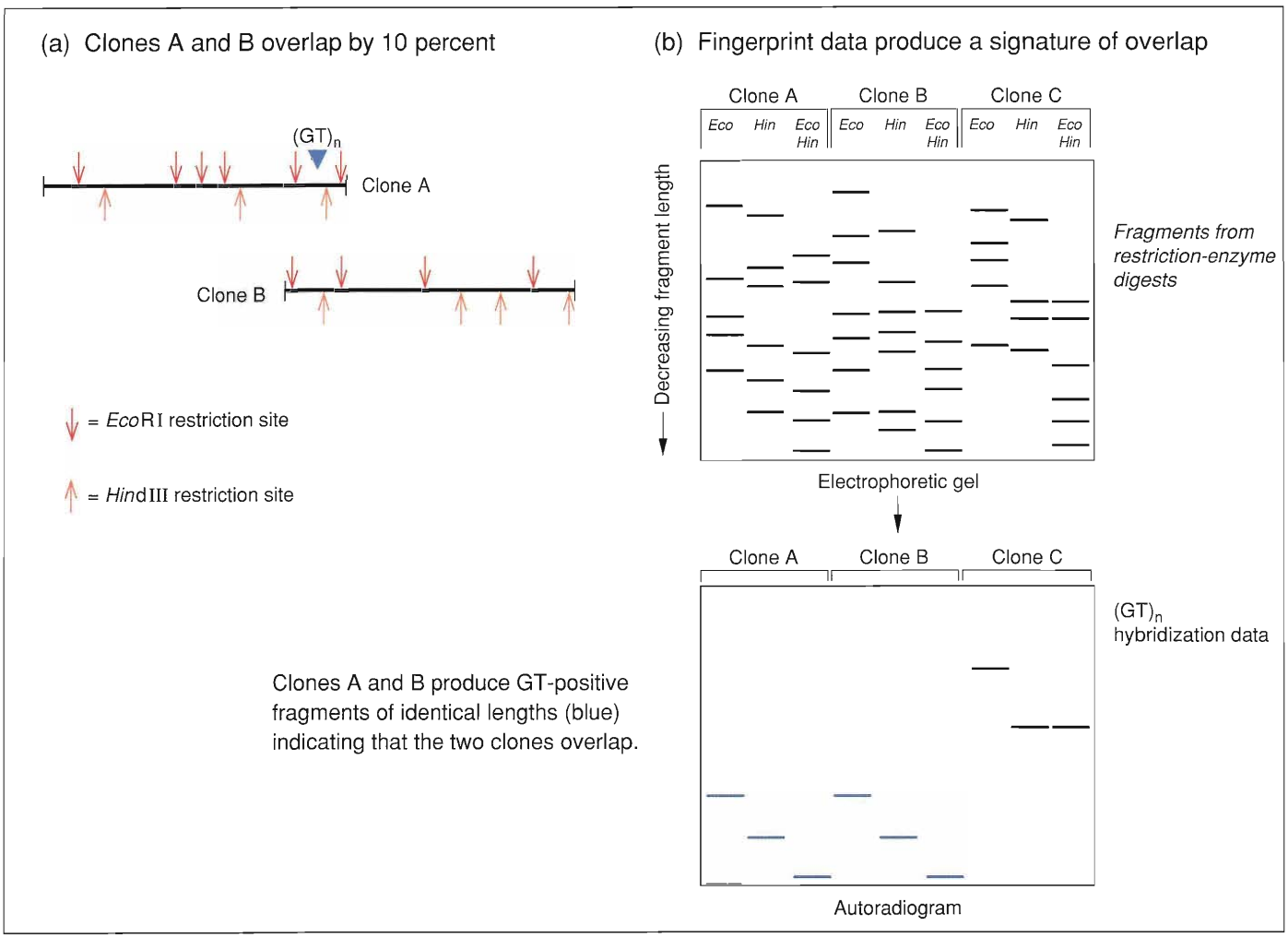


Figure 3. Detection of Small Clone Overlaps Using Repetitive-Sequence Fingerprints

Shown in (a) is a diagram of two clones, A and B, that overlap by 10 percent of their lengths. Arrows indicate restriction (cutting) sites for the restriction enzymes *Eco*RI and *Hind*III. Clones A and B each contain a single $(GT)_n$ site, which happens to occur in the short overlapping region. Shown in (b) is a diagram of the restriction-fragment fingerprints and corresponding $(GT)_{25}$ hybridization data produced from clones A and B as well as a third clone C. The identical $(GT)_n$ hybridization pattern from clones A and B is sufficient information to infer that the two clones have a very high likelihood of overlap.

such identical patterns would arise from non-overlapping clones is extremely low. In general, if two cosmid clones from our chromosome-specific library produce the same GT-hybridization pattern, they have an extremely high probability of overlapping, even if they share only one GT-positive region.

The detailed computer algorithms used to estimate the probability of clone overlap from the fingerprint data will not be presented here. Suffice it to say those algorithms are based on Bayes' theorem for conditional probabilities and use parameters for estimating errors in restriction-fragment sizes and hybridization results that were determined through detailed statistical analysis of the experimental conditions. The computer algorithms were used to examine all possible pairs of fingerprinted clones and determine the probability of overlap for each clone pair.

Assembling the Contig Map

As illustrated in "Physical Mapping—A One-Dimensional Jigsaw Puzzle," restriction-fragment fingerprint

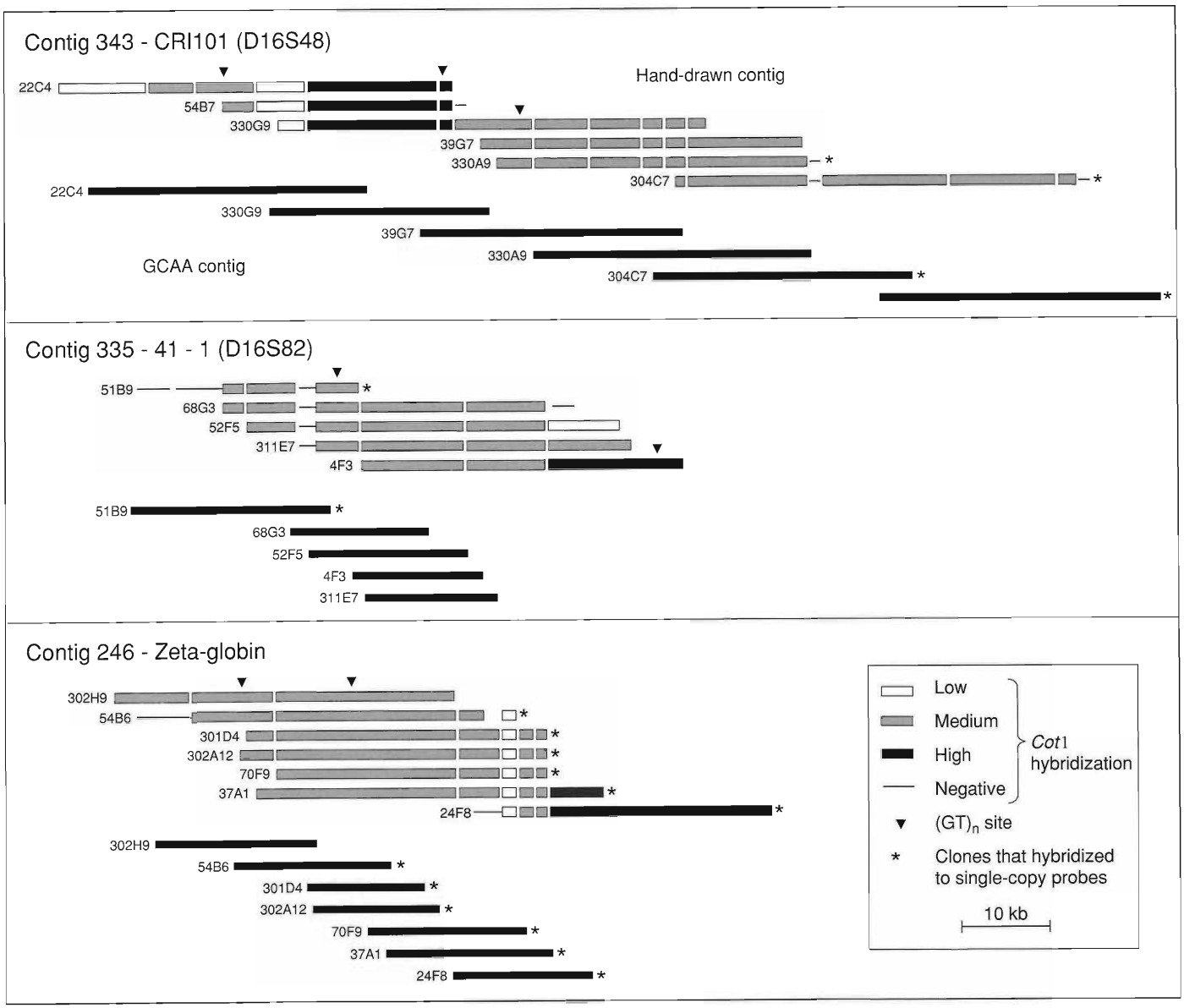


Figure 4. Comparison of Hand-drawn and Computer-generated Cosmid Contigs from Chromosome 16.
Groups of overlapping clones are arranged into contigs showing the linear arrangement and extents of clone overlap deduced from repetitive-sequence fingerprint data. The hand-drawn representations show which restriction fragments were positive for GT and *Cot* 1 hybridization probes and provides a partial ordering of the restriction fragments. The corresponding GCAA-generated contig shows the extent of overlap between clones and the contig length. Additions to GCAA are planned that will enable the algorithm to generate contigs similar to the hand-drawn contigs. As shown, the GCAA contigs sometimes differ in length from the hand-drawn contigs.

data can be used to assemble islands of contiguous, overlapping clones showing the position of each clone relative to the others and the extent of overlap between each pair of overlapping clones.

Initially we assembled contigs by sorting the output of the pairwise overlaps into sets of multiply overlapping clones. More recently Jim Fickett and Michael Cinkosky of the Laboratory's Theoretical Biology and Biophysics Group developed a "genetic algorithm" for contig assembly called GCAA, which has sped up this process considerably. The algorithm is based on optimization theory. Figure 4 compares hand-drawn cosmid contigs for chromosome 16 with versions generated by the genetic algorithm. The hand-drawn contigs are sometimes more accurate, but each one takes many hours to construct. In contrast, the computer algorithm can handle data from thousands of clones and construct hundreds of contigs automatically in a short time. It also allows manual changes to be made through interactive software. The genetic algorithm has been invaluable to our mapping efforts, as has the whole suite of informatics tools developed at Los Alamos for managing, analyzing, utilizing, and sharing mapping data. Some of those tools are described in

"Computation and the Genome Project."

About 3145 GT-positive cosmid clones and an additional 800 GT-negative cosmid clones were fingerprinted and then assembled into contigs in the manner described above. The clones formed 576 contigs with an average size of 100,000 base pairs and containing, on average, four or five clones. The largest cosmid contig spanned approximately 300,000 base pairs. These contigs cover about 58 million base pairs, or 58 percent of chromosome 16. There were also 1171 singletons (single fingerprinted clones not contained within a contig). Experiments discussed below suggest that the singletons cover 26 percent of the chromosome. Together the 4000 fingerprinted clones cover about 84 percent of chromosome 16.

If the minimum detectable overlap between clones is 50 percent of the clone lengths, the equations of Lander and Waterman suggest that one would have to fingerprint about 16,000 clones of an average length of 35,000 base pairs to reach an average contig size of 100,000 base pairs for a chromosome the length of chromosome 16. We reached an average contig size of 100,000 base pairs after fingerprinting only 4000 clones. That reduction was due to two factors. First, the repetitive-sequence fingerprints enabled the detection of clone overlaps composing between 10 and 25 percent of the clone lengths depending on the positions of the $(GT)_n$ sites. In fact, the average length of each detected overlap region was 20 percent of the clone lengths. Second, we did not fingerprint clones at random but rather preselected clones containing $(GT)_n$. By focusing our mapping efforts around regions of $(GT)_n$ sites, we effectively reduced the size of the region that was being mapped during the initial phases of mapping. These two factors resulted in the rapid construction of relatively large cosmid contigs.

Several other features are distinctive about our cosmid-fingerprinting approach. By sizing the restriction fragments from each clone, we know the extent of overlap between clones in a contig, and therefore we can estimate the length of each contig. In contrast, mapping methods that determine clone overlap from hybridization-based or STS data alone cannot determine the extent of the overlap or the length of the contigs without further analysis. Restriction-fragment lengths also provide us with information to generate partially ordered restriction maps for each contig. Finally, as a result of the GT and *Cot*1 hybridizations, we know which fragments contain GT repeats and which fragments contain *Cot*1 DNA. A GT repeat at a given site in the genome varies in length among the population and therefore provides a source of polymorphic markers for genetic-linkage mapping. Our contig map thus provides the positions of fragments containing those potential markers. The *Cot*1 hybridization is useful because fragments that do not hybridize to the *Cot*1 probe are free of the most abundant classes of repetitive DNA and are therefore likely to contain single-copy sequences, which may be candidates for genes. Finally, as the map is further developed and the repetitive-sequence distribution more accurately determined, it may reveal new insights into genome organization and the molecular evolution of mammalian chromosomes.

Evaluation of the Cosmid Contig Map

After constructing the 576 cosmid contigs, we first wanted to ascertain their distribution on chromosome 16. David Callen and Grant Sutherland in Australia located 140 of our cosmid contigs on their panel of mouse/human hybrid cells. The 50 different hybrid cells in their panel contain, in addition to the full complement of mouse chromosomes, increasingly longer portions of human chromosome 16, starting from the far end of the long arm of the chromosome (see Figure 5). In effect, the panel divides the chromosome into bins, or intervals, 1.6 million base pairs in length. They found the 140 cosmid contigs to be distributed evenly over the intervals defined by the hybrid-cell panel.

Second, to evaluate the accuracy of the contigs, we picked 19 pairs of clones from 11 different contigs and checked whether each pair that had been assigned to the same contig hybridized to the same large restriction fragment and therefore came from the same region of chromosome 16. The DNA for these experiments was isolated from a mouse/human hybrid-cell line containing human chromosome 16 only. Eight rare-cutting restriction enzymes were used to make eight different complete digests of the DNA, and the resulting large restriction fragments were separated in parallel by pulsed-field gel electrophoresis. The fragments were then blotted onto filters, and each filter was probed with one clone from each pair. This analysis confirmed that the two members of each of the 19 clone pairs came from the same region of the genome.

A second check on contig accuracy involved hybridization of 43 single-copy probes (probes containing sequences that appear only once in the human genome) to membranes containing a gridded array of our 4000 fingerprinted clones. The single-copy probes were graciously provided by a large number of collaborators and associates. Ideally, if a single-copy probe hybridizes to more than one clone, those clones should be contained within a single contig and

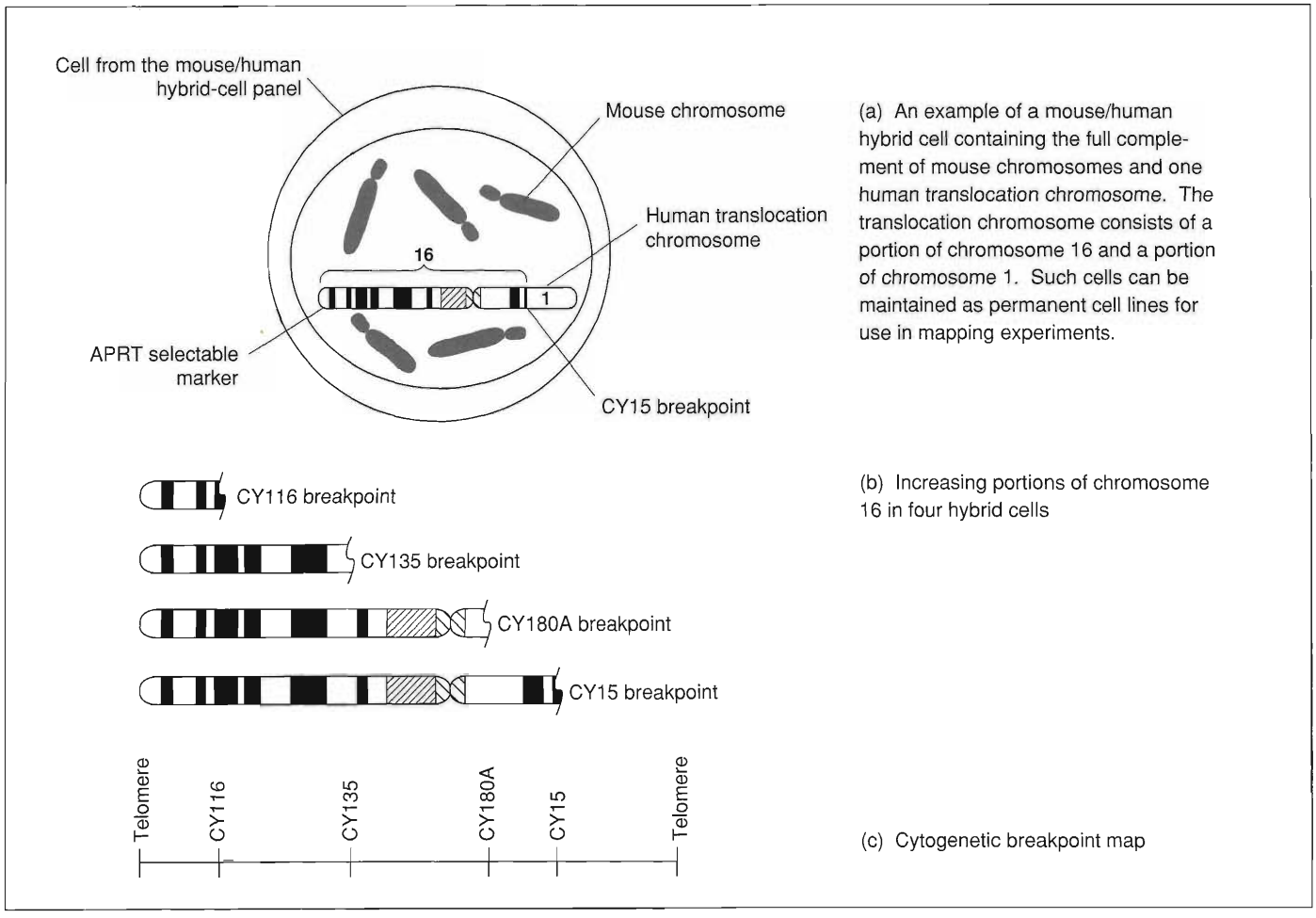


Figure 5. Hybrid-Cell Panel and the Cytogenetic Breakpoint Map for Chromosome 16

A panel of 50 different mouse/human hybrid cells, each containing an increasingly longer portion of chromosome 16 starting from the tip of the long arm of the chromosome, is a convenient tool for constructing a low-resolution physical map of the chromosome. The hybrid cells are formed by fusing mouse cells with human cells and growing them in a medium in which only those cells containing a particular gene (APRT) can survive. Thus APRT is called a selectable marker. It is near the end of the long, or q, arm of chromosome 16. During the fusion process and subsequent growth, human chromosomes that lack the selectable marker are lost, resulting in a mouse/human hybrid containing a single human chromosome 16. The 50 different hybrids were derived from a collection of patients' cells that had each undergone translocations (breakage and rejoining) of chromosome 16 with another human chromosome. (a) The type of hybrid cell produced by the fusion process and selectively grown for inclusion in the panel is shown. The hybrid cell contains the full complement of mouse chromosomes and one chromosome produced by a translocation between human chromosomes 16 and 1. Because this chromosome includes the portion of the q arm of chromosomes 16 containing APRT, it survived the fusion and selective growth process. (b) Increasing portions of chromosome 16 contained in some of the hybrid cells of the panel are shown. The panel contains 50 hybrid cells and, in effect, divides the chromosome into intervals with an average length of 1.6 million bases. Each portion ends at a so-called breakpoint of the chromosome, a natural site of chromosomal translocation. (c) A cytogenic map of chromosome 16 indicating the locations of the breakpoints in (b). The complete cytogenetic breakpoint map derived from the hybrid cell panel contains 50 breakpoints separated by intervals with an average length of 1.6 million base pairs. A human DNA probe or clone from chromosome 16 can be localized to a region between two breakpoints by showing that it hybridizes to the DNA from all hybrid cells containing that region and *does not* hybridize to the DNA from the hybrid cell in which that region is absent.

should overlap one another because they contain the same unique sequence. Our analysis showed no unequivocal false-positive overlaps in our contigs, and it also enabled us to detect overlaps between some singleton clones and our existing contigs.

The hybridizations of single-copy probes to the gridded arrays of fingerprinted clones also allowed us to estimate how much of chromosome 16 is covered by our fingerprinted clones. Out of 43 probes, 25 hybridized to clones within contigs, 11 hybridized to singletons, and 7 did not hybridize to any of the fingerprinted clones. These results suggest that our cosmid contigs cover 58 percent of chromosome 16, and the singleton cosmids cover 26 percent of the chromosome for a total coverage of 84 percent.

Our goal was to construct a map composed of at most 100 contigs, each having an average size of about a million base pairs. Having already achieved substantial coverage, we were at a point where continued random fingerprinting of cosmid clones was no longer the most efficient way to achieve this goal. At that point the likelihood of fingerprinting a new clone that was not yet represented in contigs was diminishing, while the likelihood that the new clone would fall within pre-existing contigs was increasing. The gaps between cosmid contigs could be closed by a directed approach called chromosome walking (see Figure 9 in "DNA Libraries") but to "walk" from one cosmid clone to the next would be a very slow and labor-intensive process.

Fortunately, by that time YAC technology had matured. In 1991 Mary Kay McCormick at Los Alamos successfully constructed chromosome 21-specific YAC libraries from flow-sorted chromosomes using a modified cloning technique. Eric Green and Maynard Olson at Washington University, in collaboration with Bob Moyzis and coworkers at Los Alamos, had developed a substantial number of STS markers for chromosome 7 from our chromosome 7-specific library of M13 clones (a library of cloned single-stranded DNA fragments for sequencing). They thereby demonstrated the feasibility of generating large numbers of STS markers for use in physical mapping.

Green and Olson had already used STS-content mapping to construct a contig of YAC clones covering the region surrounding the cystic-fibrosis gene. In particular, they had developed a set of STS markers from pre-existing genetic-linkage markers, which had been used to find the gene, and from cDNAs for sequences within the cystic-fibrosis gene. Then they used those STSs to screen a YAC library made from total-genomic human DNA and pick out the YAC clones containing each marker. Two YACs that contain the same STS marker must overlap because each STS is a unique sequence that has been shown to appear only once on the genome. Thus, based on the STSs contained in each YAC, they were able to construct a contig of overlapping YAC clones spanning about 1.5 million base pairs and containing the cystic-fibrosis gene.

These advances made it feasible for us to consider closing the gaps in our cosmid contig map with YAC clones from chromosome 16. We decided that the most efficient strategy would be to work with a chromosome 16-specific YAC library.

Improving YAC Cloning Techniques

YACs are cloning vectors that replicate as chromosomes in yeast cells and can accommodate human DNA inserts as large as 1 million base pairs. These large inserts are extremely useful for attaining long-range continuity in contig maps, and therefore the use of YAC clones in large-scale mapping of the human genome was becoming widely adopted by 1990.

From our point of view, however, prior to McCormick's work at Los Alamos on improving YAC cloning techniques, YAC cloning had some serious drawbacks. First, large amounts of human DNA were required to construct YAC clone libraries because the efficiency of transforming yeast cells by the addition of a YAC clone was relatively low. Consequently, creating a chromosome 16-specific library of YAC clones from the small DNA samples obtained by sorting chromosomes would be difficult if not impossible.

Second, we knew that 30 to 50 percent of the clones in most YAC libraries were chimeric, that is, they contained DNA from two or more nonadjacent regions of the genome. Such clones can be produced when more than one YAC or partial YAC recombinant molecule enters a yeast cell, and, during the transforming process, the human DNA inserts in these recombinant molecules recombine with each other to produce a YAC containing two different human inserts instead of only one. Chimeras are also produced when two DNA fragments are accidentally ligated prior to their ligation with the vector arms of the yeast artificial chromosome.

Chimeric YACs can be identified during the construction of contig maps, but when a large percentage of clones in a YAC clone library are chimeric, the difficulty of map construction increases considerably and the process is error-prone.

These two major difficulties were overcome in 1991 when McCormick succeeded in constructing a chromosome 21-specific YAC library from sorted chromosomes. Not only was she able to work with small amounts of DNA but

also only a few percent of the resulting clones are chimeric. The modified cloning techniques she developed to accomplish this technical tour de force are described in "Libraries from Flow-sorted Chromosomes." Following this breakthrough, McCormick applied the new YAC-cloning techniques to the construction of a chromosome 16-specific YAC library for specific use in our mapping effort.

Closing Gaps in the Contig Map with YACs

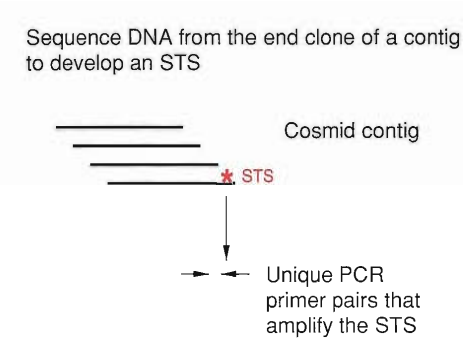
The YAC library for chromosome 16 contains about 550 clones, and the clones contain inserts with an average size of 215,000 base pairs. Assuming that our 576 cosmid contigs are randomly distributed over chromosome 16, we estimate that the average gap between cosmid contigs is 65,000 base pairs. Thus each gap should be closed with a single YAC clone. Figure 6 outlines our procedure for incorporating YAC clones into the cosmid contig map. We first develop STS markers from the end clones of our cosmid contigs. We then use PCR-based screening to pick out YAC clones that contain each STS and therefore overlap with the cosmid contig from which the STS was derived. Details of this work are presented in "The Polymerase Chain Reaction and Sequence-Tagged Sites" in "Mapping the Genome," and the design of the pooling scheme used to screen the YAC library is described in an accompanying sidebar "YAC Library Pooling Scheme for PCR-based Screening."

Figure 7 presents the results of screening the library for one STS. To date, we have made 89 STS markers from end clones of cosmid contigs and have incorporated 30 YAC clones into the contig map by showing that they contain STSs derived from those end clones.

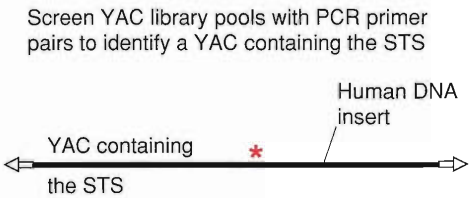
Figure 6. YAC Closure of Gaps in the Cosmid Contig Map

Both STS markers and YAC inter-Alu PCR products are being used to identify overlaps between chromosome 16 YAC clones and our cosmid contigs. The procedure is outlined below.

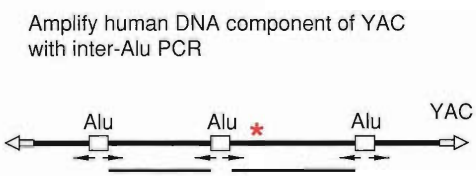
(a) Sequence-tagged sties (STSs) are generated from the end clones of cosmid contigs. This involves sequencing about 300 base pairs from the end clone, identifying a pair of candidate primer sequences, synthesizing the primers, and checking that the two primers, when used in the polymerase chain reaction, will amplify a single region of the genome. If so, the amplified region is an STS.



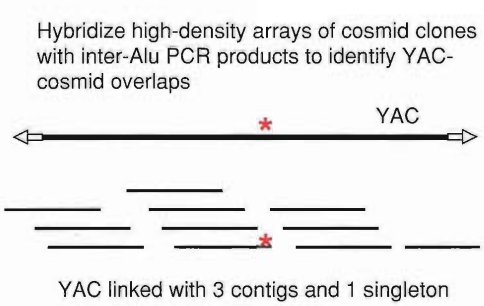
(b) YAC clones containing the STS are identified by PCR-based screening of pools of YAC clones from our chromosome 16-specific YAC library. A YAC containing the STS must overlap the cosmid clone from which the STS was derived. Figure 8 illustrates the steps in the screening process.



(c) To identify all cosmid clones that overlap with a YAC, inter-Alu PCR products are generated from each YAC and labeled for use as a hybridization probe. (Note that the inter-Alu products represent only a portion of the human insert in the YAC clones.)



(d) The probe is then hybridized to membranes containing high-density arrays of fingerprinted cosmid clones. Cosmid clones that yield positive hybridization signals must overlap the YAC. A single YAC often overlaps several cosmid contigs, as shown in the figure. However, the hybridization data do not determine the relative positions of the cosmid contigs.



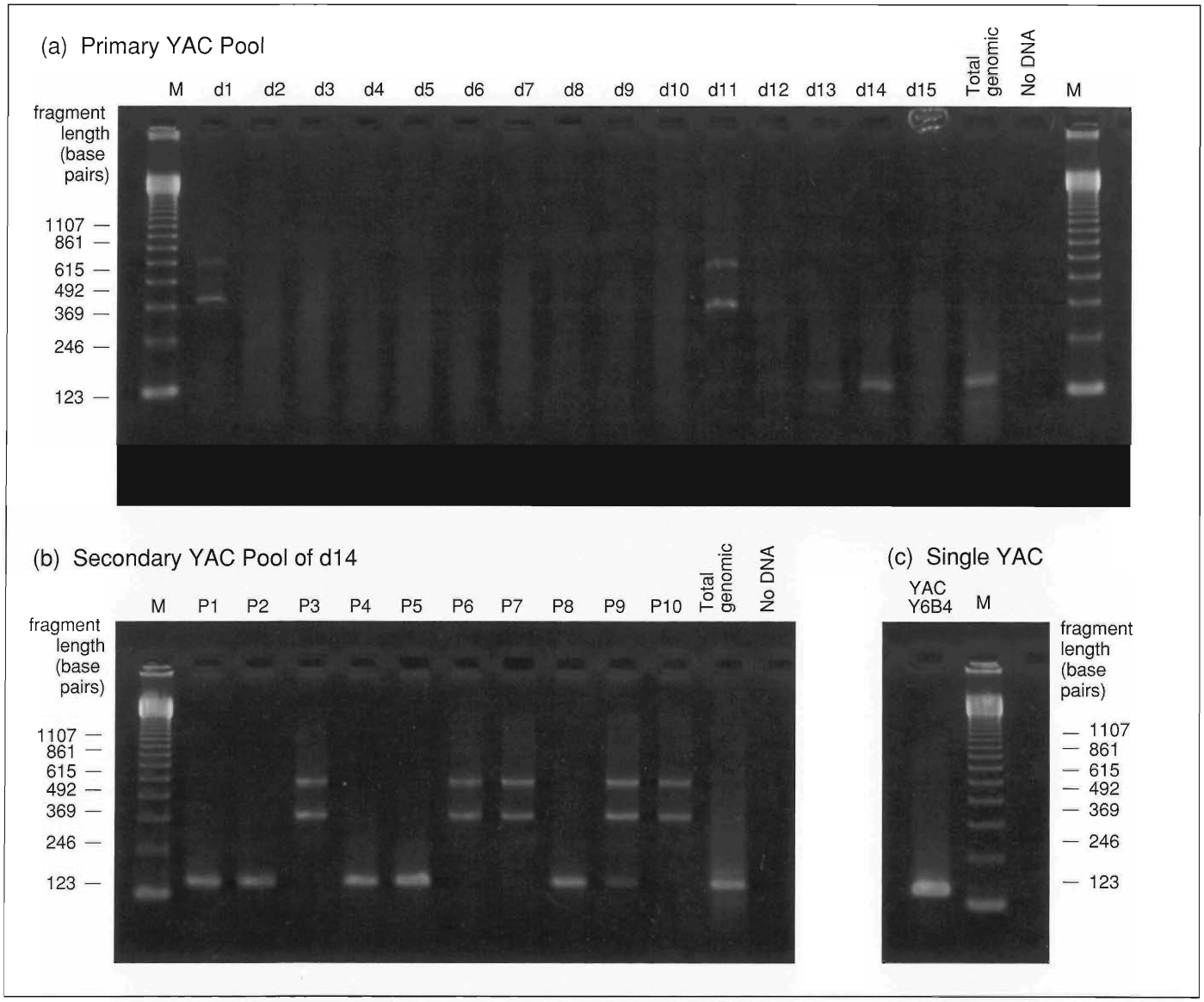


Figure 7. PCR-based Screening of YAC Library Pools for Clones Containing an STS

Our library of 540 YACs was divided into 15 sets of 36 YACs each. These 15 sets are called the primary pools, or detectors, and are numbered d1 through d15. The 36 YACs in each primary pool are then divided into 10 secondary pools (p1 through p10) according to David Torney's design for the 1-detector (see "YAC Library Pooling Scheme for PCR-based Screening" in "Mapping the Genome"). Each of the 36 YACs occur in 5 pools of the 1-detector. (a) An electrophoretic gel in which the PCR products produced by screening the primary pools for STS 25H11 have been separated by length. The lane third from the right, marked "total genomic DNA," contains the STS 25H11, which was amplified from total-genomic human DNA. In this experiment only detector 14 produced a PCR product that has the same length as STS 25H11. Multiple bands at different lengths in lanes d1 and d11 indicate PCR amplification of regions other than STS 25H11 and can therefore be ignored. (b) To determine which YAC was responsible for the positive signal from primary pool d14, we screen the 10 secondary pools composing the 1-detector for d14. Five of these pools, p1, p2, p4, p5, and p8, were identified as positive for STS 25H11. YAC clone Y6B4 was the only YAC that occurred in each of these five pools. (Multiple bands in p3, p6, p7, p9, and p10 were again the result of spurious PCR amplification and did not match the length of STS 25H11.) (c) Finally, the PCR was run on YAC Y6B4 only. The results confirm that this YAC contains STS 25H11. This pooling strategy allows error correction of false negatives in the secondary pools. If less than five positives were identified, this would increase the number of likely candidate YACs that could then be individually checked to find the correct YAC. In other pooling strategies, false negatives lead to the loss of YAC candidates.

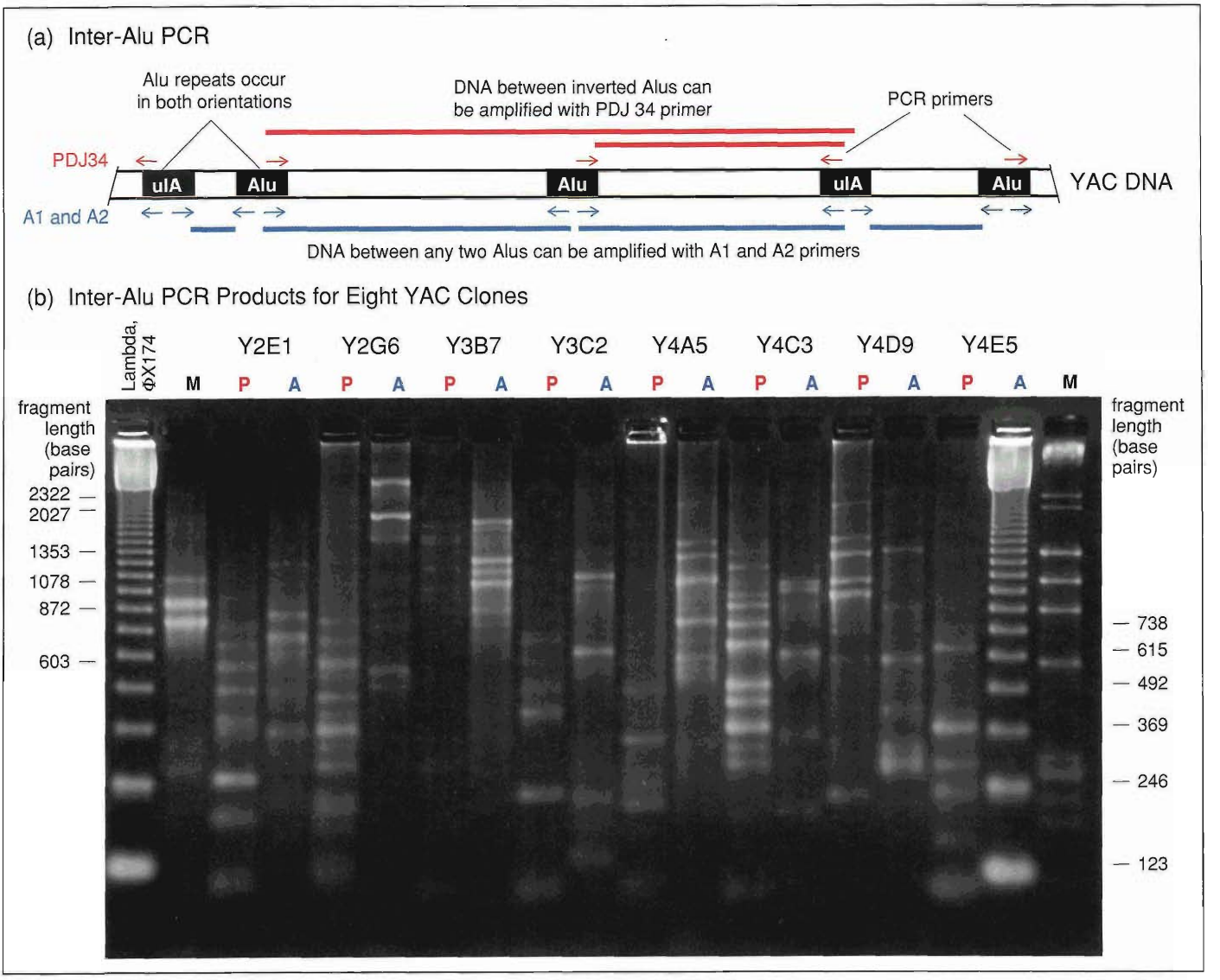


Figure 8. Inter-Alu PCR Amplification of DNA from YAC Clones

(a) Primers whose sequences match the ends of the Alu repetitive sequence can be used in the polymerase chain reaction to amplify the DNA occurring between of Alu sequences in the human DNA insert of a YAC clone. Alu sequences are 300 base pairs long, occur on average at intervals of 3300 base pairs in the human genome and are absent from the yeast genome. As shown in the figure, Alu sequences can be oriented in opposite directions along the DNA in the genome. The figure shows two sets of Alu primers. Those marked PDJ34 match only one end of the Alu sequence and therefore can amplify DNA between Alu sequences of opposite orientation. Primers A1 and A2 match either end of the Alu sequence and therefore can amplify DNA between any two Alu sequences. The polymerase chain reaction can be used to amplify regions up to several thousand base pairs in length. (b) Agarose gel containing inter-Alu PCR products of YAC clones. Alu primers PDJ34 (from Pieter de Jong, LLNL) or A1 and A2 (from Michael Scicillano, M.D., Anderson Hospital) were used in the PCR to amplify human DNA from eight different YAC clones and the amplified products were separated by electrophoresis on eight lanes of the gel shown in the figure. The first two and last lanes contain fragments of known lengths and are used to calibrate the lengths of the PCR products. Inter-Alu PCR products range in size from 100 base pairs to greater than 2500 base pairs. Each of the YACs shown yielded from 5 to 15 such PCR products.

Table 2. Results of Hybridization of Inter-Alu PCR Products to YACs

Number of cosmid contigs overlapped by a single YAC	0	1	2	3	4	5	6	>6
Number of YACs	105	133	84	41	24	12	6	6

Each YAC clone has an average insert size of 215,000 base pairs, so we expect many of them will bridge the gaps between two or more cosmid contigs. To find those contigs, we adopted a hybridization strategy which is less time-consuming than the STS approach. YAC clones are not good hybridization probes for detecting overlaps between human DNA inserts because the yeast DNA in those clones contains sequences that are homologous to human DNA and can produce false-positive hybridization signals. We need, instead, to generate DNA probes from each YAC clone that we know are derived from the human DNA insert in that clone. An efficient procedure, known as inter-Alu PCR, is outlined in Figure 8(a). The procedure uses the polymerase chain reaction to amplify DNA that lies between Alu sequences within the human DNA insert of the YAC. Alu sequences are found in human DNA but not in yeast DNA. Therefore, if primers from the ends of the Alu sequence are used in the polymerase chain reaction, the reaction will amplify regions of the human DNA insert only. Figure 8(b) shows a gel containing the amplified products derived by applying inter-Alu PCR to each of eight YAC clones. Each lane of the gel contains PCR products from one YAC clone. The average number of PCR products was about six.

The inter-Alu PCR products from each YAC clone were then radiolabeled with ^{32}P nucleotides and annealed with *Cot*1 DNA, a process that covers any *Cot*1 repetitive sequences that might be present. The PCR products were then ready to be used as a hybridization probe to screen the 4000 fingerprinted cosmid clones. To facilitate screening, the 4000 fingerprinted clones were fixed on membranes in a high-density, gridded array. Each membrane accommodates 1536 clones, so the entire set of fingerprinted cosmid clones was arrayed on three membranes (see Figure 9). Cosmids that yield positive hybridization signals must contain a DNA sequence present in the YAC clone from which the hybridization

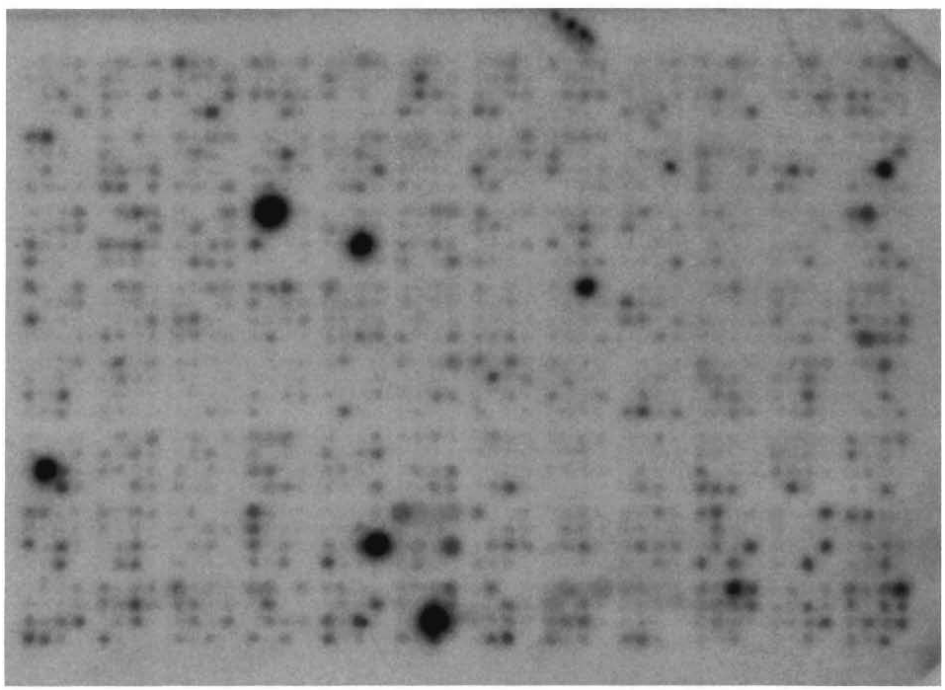
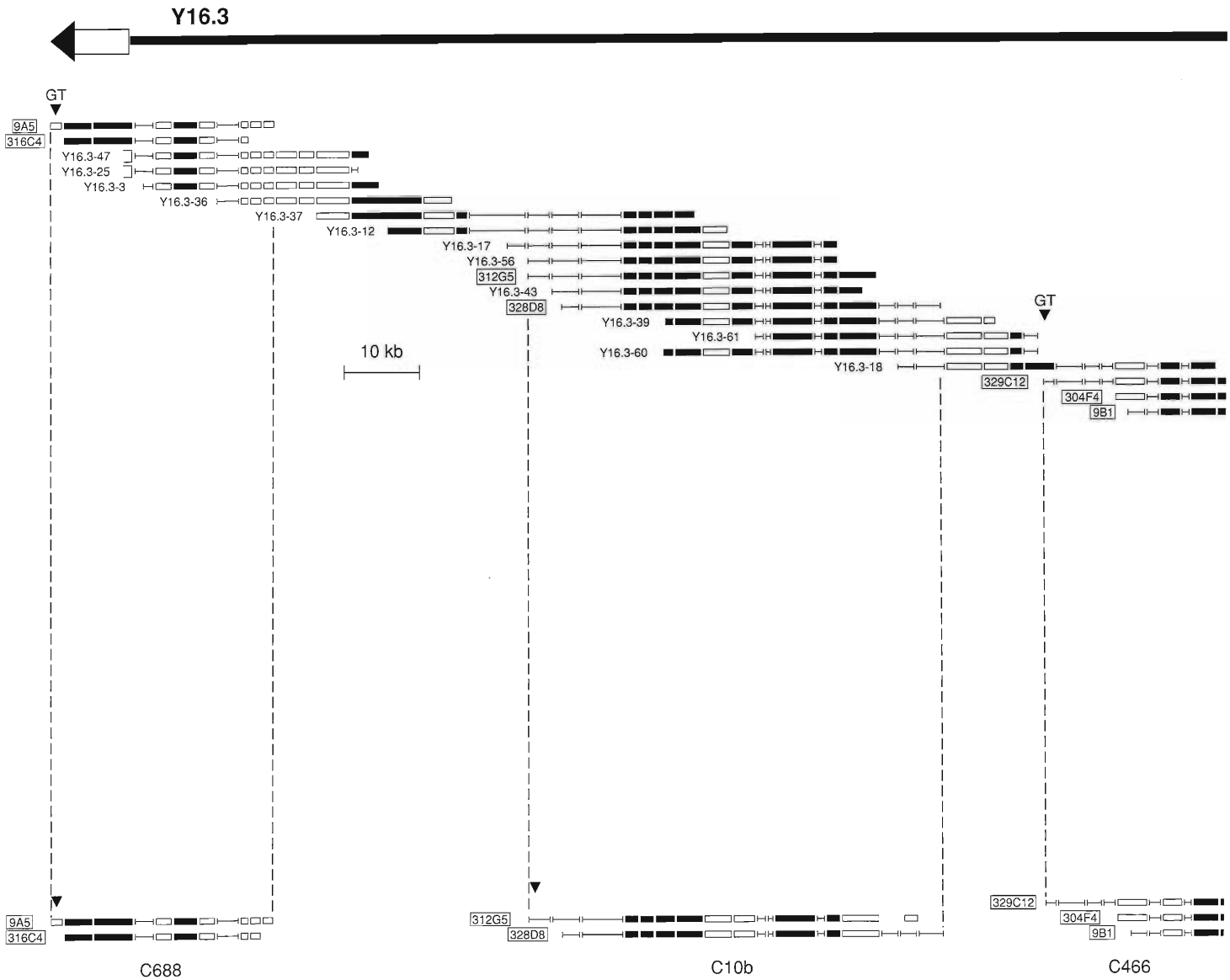


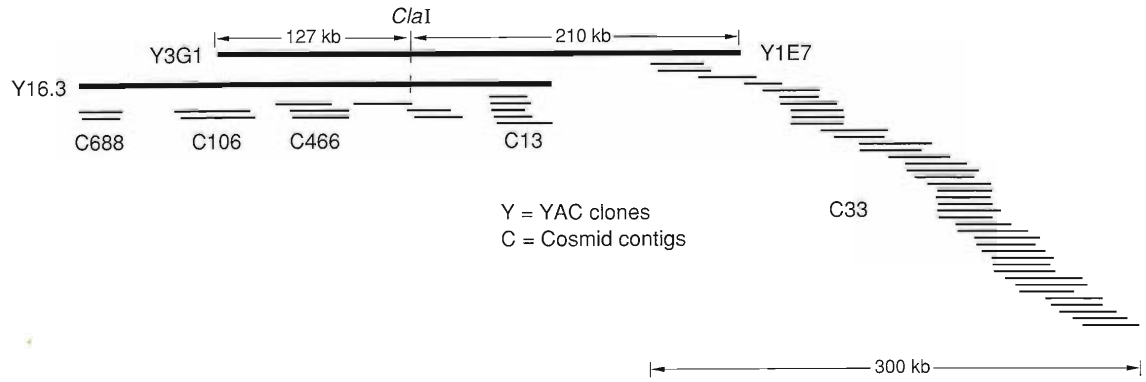
Figure 9. Hybridization of Inter-Alu PCR Products to Cosmid Clones

The figure shows an autoradiogram of a membrane containing 1536 cosmid clones. The clones from the wells of 16 different microtiter plates (8 rows and 12 columns for 96 clones per plate) were stamped onto a membrane the size of the microtiter plate by a high-precision robotic device. The resulting gridded array of clones provides a convenient tool for hybridization experiments. The darker and larger dots are the result of hybridization of YAC inter-Alu PCR products to specific cosmid clones. Here the PCR products from YAC clone Y3A12 hybridized to cosmid clones from 2 different contigs. The results suggest that the YAC clone overlaps those cosmid contigs. The automated robotic gridding device that makes the hybridization grids was designed and built by Pat Medvick, Tony Beugelsdijk, and Bob Hollen in the MEE-3 group. A photograph of the device appears on the opening pages of "DNA Libraries" and is discussed in "Libraries from Flow-sorted Chromosomes."

(a) Subcloning of YAC 16.3



(b) YAC-cosmid contig



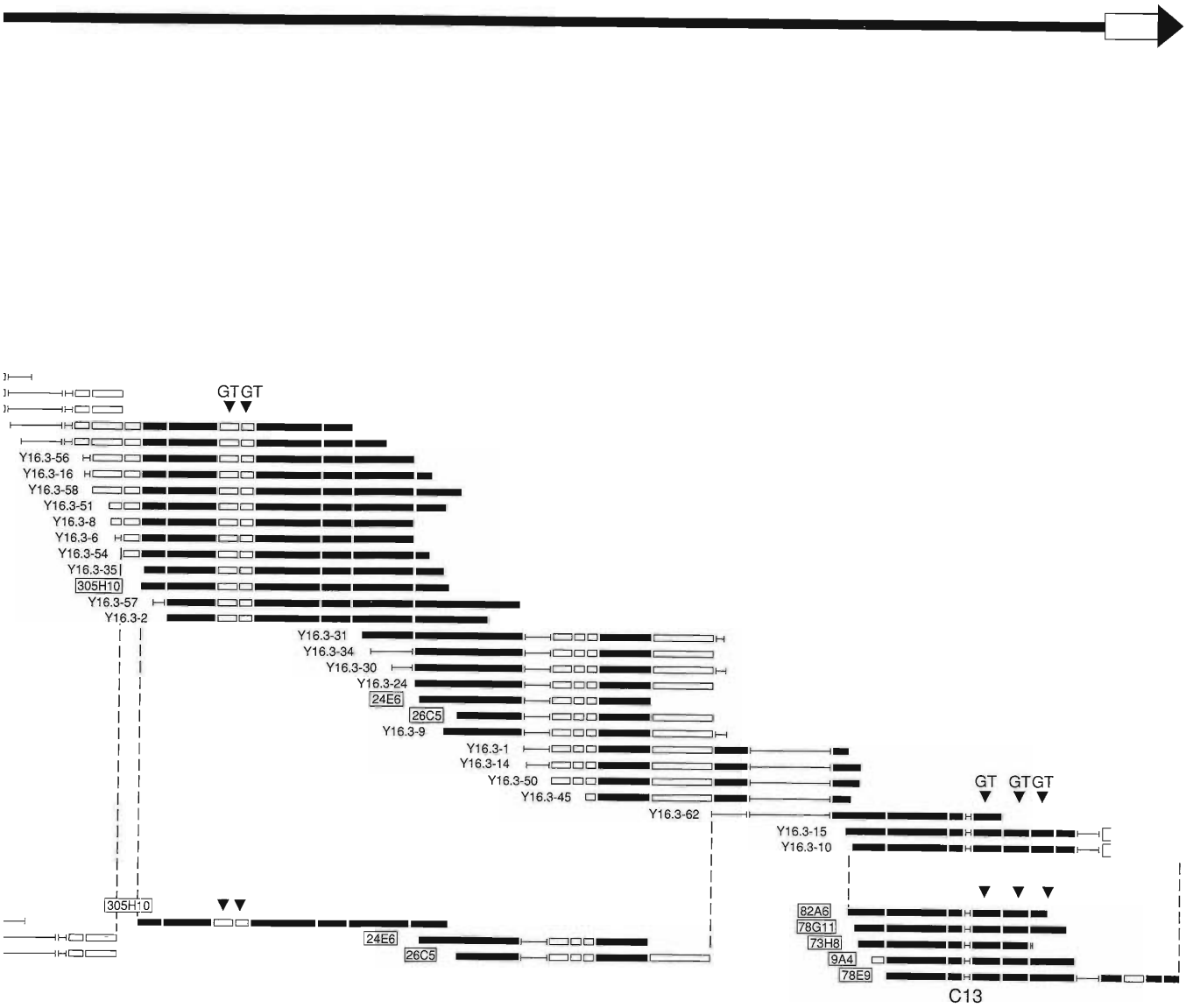
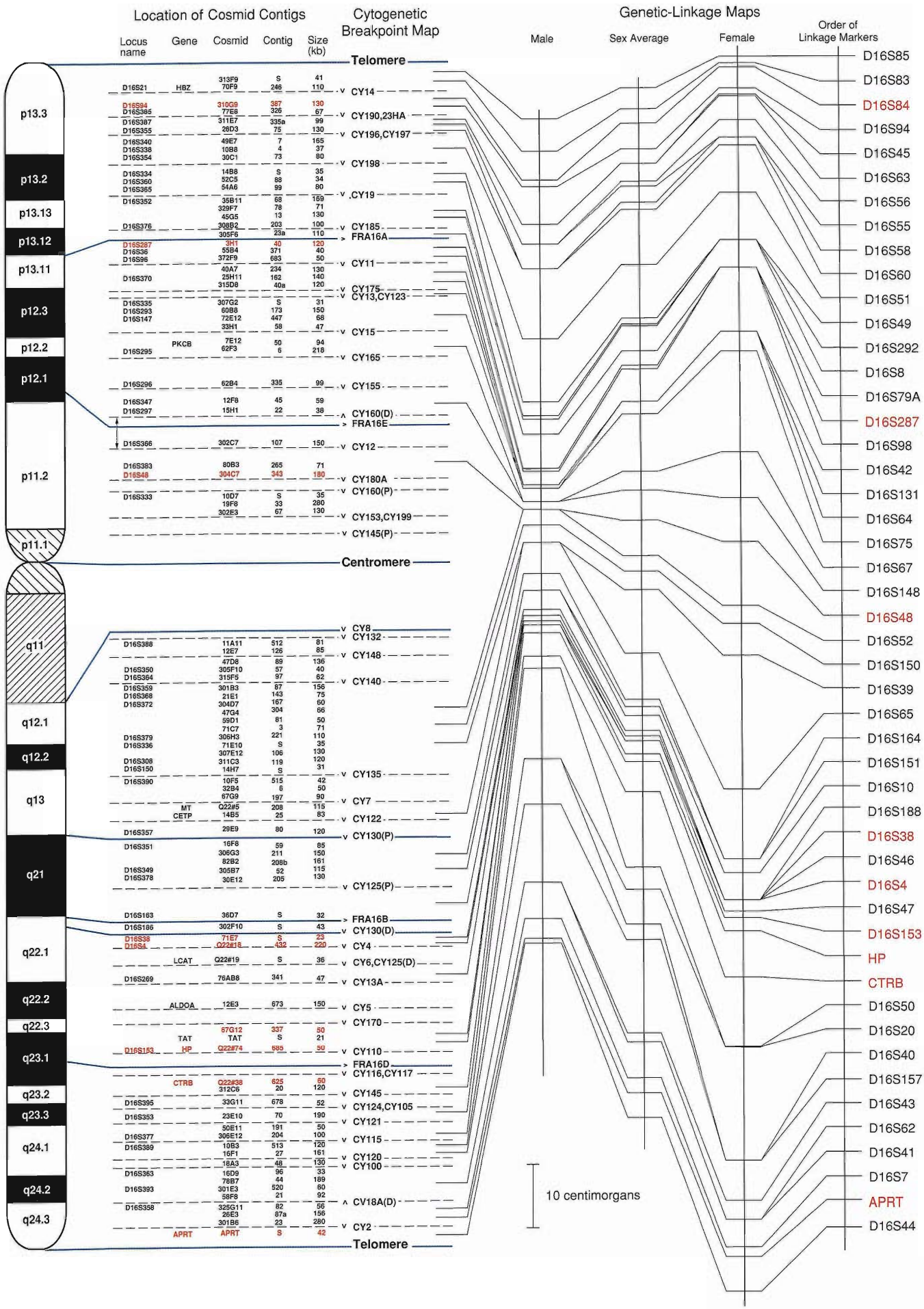


Figure 10. Confirmation of YAC-Cosmid Overlaps by YAC Subcloning

Hybridization experiments using inter-Alu PCR products from YAC clone Y16.3 suggested that this clone bridges the gaps between four cosmid contigs. To confirm that result, Y16.3 was subcloned into cosmid vectors and, as shown in (a), the resulting cosmid subclones were fingerprinted and assembled into a contig spanning the YAC. Five cosmid contigs from our chromosome 16 map were then aligned with the YAC subclone contig, based on their repetitive-sequence fingerprints. These results confirm the overlaps deduced from the hybridization experiments. Overlap of Y16.3 with an additional contig, C688, was detected by repetitive-sequence fingerprinting of the cosmid subclones of Y16.3. Thus, four out of five cosmid contigs that overlap this YAC were detected by the hybridization of inter-Alu PCR products to the high-density arrays of fingerprinted cosmid clones. (b) Other hybridization experiments have indicated overlaps with two other YACs and a sixth cosmid contig. Together these three YACs and six cosmids cover over 600,000 base pairs in chromosome 16.


Location of Cosmid Contigs
Cytogenetic Breakpoint Map
Genetic-Linkage Maps
Locus name
Gene
Cosmid
Contig
Size (kb)
Male
Sex Average
Female
Order of Linkage Markers
Telomere
Centromere
p13.3
p13.2
p13.13
p13.12
p13.11
p12.3
p12.2
p12.1
p11.2
p11.1
q11
q12.1
q12.2
q13
q21
q22.1
q22.2
q22.3
q23.1
q23.2
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q24.2
q24.3
D16S85
D16S83
D16S84
D16S94
D16S45
D16S63
D16S56
D16S55
D16S58
D16S60
D16S51
D16S49
D16S292
D16S8
D16S79A
D16S287
D16S98
D16S42
D16S131
D16S64
D16S75
D16S67
D16S148
D16S48
D16S52
D16S150
D16S39
D16S65
D16S164
D16S151
D16S10
D16S188
D16S38
D16S46
D16S4
D16S47
D16S153
HP
CTRB
D16S50
D16S20
D16S40
D16S157
D16S43
D16S62
D16S41
D16S7
APRT
D16S44
10 centimorgans

probe was derived. Consequently, the cosmid clone is highly likely to overlap the YAC clone.

To date we have generated inter-Alu PCR products from 411 YAC clones and hybridized those products to the arrays of fingerprinted cosmid clones. As shown in Figure 9, the inter-Alu products yield intense hybridization signals. The hybridization results enabled us to incorporate 334 YAC clones into our cosmid contig map. The PCR products from 133 YAC clones showed overlap with only a single cosmid contig and therefore extended those contigs but did not close any gaps in the map. Other YACs were shown to overlap as many as six separate cosmid contigs. Table 2 (page 199) lists the number of YACs whose PCR products hybridized to clones in one, two, three, four, five, or more than five cosmid contigs. The hybridization results also enabled us to join 203 singletons into the YAC-cosmid contigs. The number of YAC cosmid contigs in our map is now 462, and the average contig size has grown from 100,000 base pairs to 218,000 base pairs. The total number of "islands" in the map (462 YAC-cosmid contigs plus 54 YAC singletons) cover 94 percent of chromosome 16. Overlaps between YAC and cosmid clones were detected by hybridization of YAC inter-Alu PCR products to cosmid clones.

Verification of YAC-Cosmid Contigs

Our implicit assumption in the discussion above was that if the inter-Alu PCR products from a YAC hybridize to a cosmid clone, the human DNA insert in the YAC clone overlaps the human insert in the cosmid clone, and thus the two are from the same region of chromosome 16. However, we have discovered that chromosome 16 contains a number of low-abundance repetitive sequences (see "What's Different about Chromosome 16?"). Those repetitive sequences would not have been masked by annealing the PCR products with *Cot*1 repetitive DNA prior to hybridization. Therefore, if the inter-Alu PCR products from a YAC clone contain those low-abundance repeats, they would hybridize to cosmid clones that did not necessarily overlap the YAC clone. Consequently, we used an independent method to confirm the inferred overlaps between YACs and cosmid contigs.

Our procedure involved subcloning the DNA insert in each of seven YAC clones into cosmid vectors, generating a repetitive-sequence fingerprint for each of the resulting cosmid subclones, and comparing the fingerprints of the subclones to each other and to the fingerprints of the original set of fingerprinted cosmid clones to detect overlaps. Figure 10(a) shows how the cosmid subclones of YAC 16.3 overlapped among themselves and linked up with members of our original set of fingerprinted cosmid clones. Hybridization of inter-Alu PCR products had indicated that the YAC 16.3 clone overlapped four cosmid contigs. The results of subcloning the YAC confirmed the hybridization results. Two more YAC clones were found to overlap this region based on hybridization of their inter-Alu PCR products. This YAC-cosmid contig currently contains two of these YACs and six cosmid contigs, and

Figure 11. The Integration of Physical and Genetic-Linkage Maps of Chromosome 16

Physical and genetic-linkage mapping data presently available for chromosome 16 are summarized in the figure on this spread. Together they provide a resource for isolating a variety of genes on the chromosome. At right are three genetic-linkage maps showing genetic distances (in centimorgans) of 49 polymorphic DNA markers derived from male, female, and sex-averaged linkage data. These data were compiled by the Second International Workshop on Human Chromosome 16 and are based on analysis of pedigrees in CEPH (Centre d'Etude du Polymorphisme Humain). The coordinates of the physical mapping data are defined by (1) the cytogenetic map showing the dark and light Giemsa-stained bands of chromosome 16; and (2) the cytogenetic breakpoint map, the set of fifty horizontal lines that are positioned along the chromosome bands at the fifty breakpoints of chromosome 16 determined from the mouse/human hybrid-cell panel (see Figure 6). A cosmid clone from our contig map can be localized to a region or interval between two breakpoints by showing that it is present in the DNA of hybrid cells containing the chromosomal region corresponding to that interval but absent in the DNA of hybrid cells lacking that region. Each of 140 cosmids, and thus the contigs in which they reside, have now been placed into one of the 50 intervals. The YACs that overlap those 140 contigs are thereby regionally localized as well. The DNA in the cosmid contigs and YACs that have been located on the breakpoint map covers 21 million base pairs, or about 21 percent of the chromosome. In a separate effort, polymorphic DNA markers from the linkage map have been located onto the breakpoint map thereby integrating the linkage map with the cytogenetic breakpoint map and with the cosmid contigs located on the breakpoint map. We have also integrated the linkage map directly with our cosmid contigs by hybridizing 50 gene and polymorphic DNA markers to our high-density arrays of fingerprinted clones and identifying which clones contain those genes and markers. Shown in red are cosmids that have been both regionally localized and shown to contain a marker from the linkage map.

it spans a region over 600,000 base pairs long [see Figure 10(b)]. In most instances the overlaps inferred from the hybridization of YAC inter-Alu PCR products were confirmed by the analysis of YAC subclones. In one instance, the inter-Alu PCR products contained a low-abundance repeat and produced a false YAC-cosmid overlap. Such false overlaps can be avoided by mapping the locations of these low-abundance repeats. Additional experiments showed that 85 to 90 percent of the cosmids that overlap a YAC are identified by the hybridization of YAC inter-Alu PCR products. In general, our verification experiments suggest that YAC inter-Alu PCR products provide convenient and reliable probes for integrating YACs into cosmid contig maps.

Integration of the Physical Map with the Genetic-Linkage Map

As discussed in Part I of "Mapping the Genome," genetic-linkage analysis with polymorphic DNA markers is often the only way to find the approximate location of genes that cause inherited disorders. The polymorphic DNA markers that are tightly linked to, or usually co-inherited with, certain diseases are located close to the causative gene (see "Modern Linkage Mapping"). To find the gene, those markers must be located on a contig map and the cloned DNA in the neighborhood of the markers can then be searched for the causative gene. In other words, the genetic-linkage map must be integrated with the physical map.

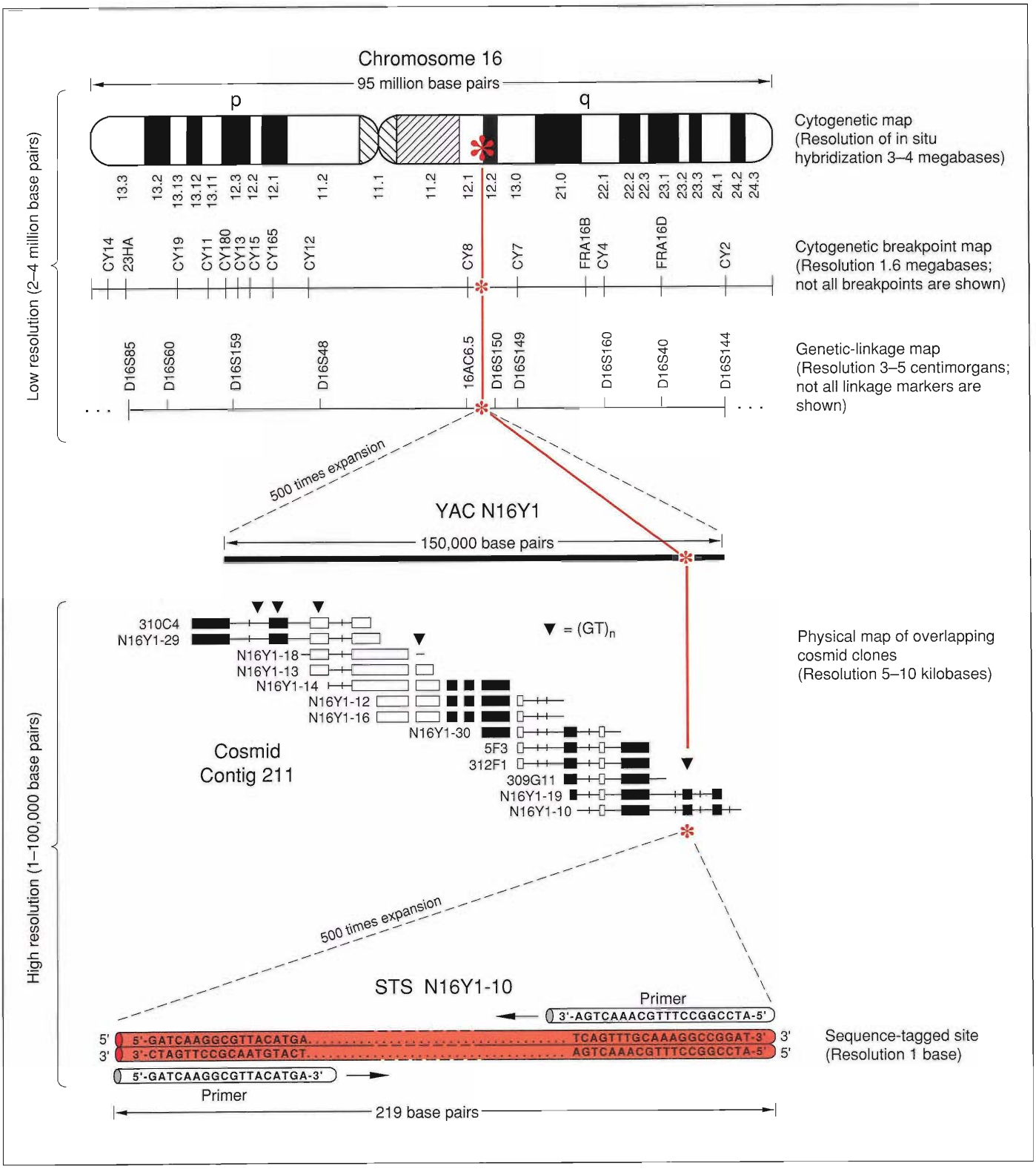
Although our contig map is not yet complete, we have been locating previously cloned genes and polymorphic DNA markers on our cosmid contigs. Here, again, the high-density arrays of fingerprinted cosmid clones are an invaluable resource. Gene and DNA-marker probes are radioactively labeled and hybridized to these arrays to determine which cosmids contain those genes or markers. Alternatively, if a gene or marker exists in a cosmid from another library, we can fingerprint that clone to integrate it with our existing contigs. Using both of these approaches, we have now located more than 50 genes and DNA markers on cosmid contigs, thereby integrating our cosmid contigs with genetic-linkage maps.

Earlier we mentioned that 140 contigs have also been localized to intervals between breakpoints on the cytogenetic breakpoint map of chromosome 16 derived from the panel of 50 mouse/human hybrid cells (see Figure 5). In addition, hybridization experiments show that inter-Alu products from 82 YAC clones overlap those localized contigs. The YAC clones and cosmid contigs now localized to intervals on chromosome 16 cover 21.4 million base pairs. Figure 11 summarizes the integration achieved so far between the linkage maps, the cytogenetic breakpoint map, and our cosmid contig map.

Application of the Map toward the Isolation of Disease Genes. The integrated maps provide potent resources to identify, isolate, and sequence regions

Figure 12. Chromosome-16 Maps at Different Levels of Resolution

Maps of chromosome 16 are being made by several different techniques and at a wide range of resolutions. The figure shows only a few of the landmarks on each map and also indicates the level of resolution presently available for each. The three low-resolution maps include a cytogenetic map, the hybrid-cell, or cytogenetic-breakpoint map, and the genetic-linkage map. At higher resolution is the cosmid contig map, which presently consists of separate contigs that are being connected by YAC clones. At the highest level of resolution, which is the sequences of bases in the genome, STSs are being generated to serve as unique physical landmarks. These landmarks can be located on all physical maps at all levels of resolution. The position of STS N16Y1-10 is traced from one level of resolution to another. It can be amplified, or duplicated millions of times, by the polymerase chain reaction using the two unique primers shown at the bottom of figure. At the top of the figure is shown the position of the STS (red) determined by in-situ hybridization to cosmid clones from which the STS was derived. In-situ hybridization localizes the STS to a region 3 to 4 million bases in length in bands 16q12.1 and 16q12.2. The STS is also shown regionally localized to the interval between breakpoints CY7 and CY8 on the hybrid-cell cytogenetic map. The intervals on this map have an average size of 1.6 million bases. The particular STS shown is not polymorphic, and therefore it cannot be located on the genetic-linkage map through linkage analysis. However, the DNA markers on the linkage map have been regionally localized on the hybrid-cell map. The alignment between the two maps allows us to infer that the STS lies between markers 16AC6.5 and D16S150 on the genetic-linkage map. The next higher level of resolution is provided by contig maps of overlapping cloned fragments. The figure shows a YAC clone containing the STS as well as a cosmid contig from which the STS was derived. The YAC clone must overlap the cosmid contig because they both contain the same STS. The position of the YAC relative to the cosmid contig is known because all inter-Alu PCR products from the YAC clone hybridized to all clones in the cosmid contig. The STS was derived from the right end clone of the cosmid contig. The information at the highest level of resolution is the base sequence of the STS determined in the process of developing the PCR protocol that recognizes and amplifies this sequence whenever it appears in a DNA sample.


Chromosome 16
95 million base pairs
p
q
Low resolution (2–4 million base pairs)
Cytogenetic map
(Resolution of in situ hybridization 3–4 megabases)
13.3 13.2 13.13 13.12 13.11 12.3 12.2 12.1 11.2 11.1 11.2 12.1 12.2 13.0 21.0 22.1 22.2 22.3 23.1 23.2 23.3 24.1 24.2 24.3
CY14 23HA CY19 CY11 CY180 CY13 CY15 CY165 CY12 CY8 CY7 FRA16B CY4 FRA16D CY2
Cytogenetic breakpoint map
(Resolution 1.6 megabases; not all breakpoints are shown)
D16S85 D16S60 D16S159 D16S48 16AC6.5 D16S150 D16S149 D16S160 D16S40 D16S144
Genetic-linkage map
(Resolution 3–5 centimorgans; not all linkage markers are shown)
500 times expansion
YAC N16Y1
150,000 base pairs
High resolution (1–100,000 base pairs)
310C4
N16Y1-29
N16Y1-18
N16Y1-13
N16Y1-14
N16Y1-12
N16Y1-16
N16Y1-30
5F3
312F1
309G11
N16Y1-19
N16Y1-10
▼ = (GT)n
Cosmid Contig 211
Physical map of overlapping cosmid clones
(Resolution 5–10 kilobases)
500 times expansion
STS N16Y1-10
Primer
3'-AGTCAAACGTTTCCGGCCTA-5'
5' 5'-GATCAAGGCGTTACATGA.....TCAGTTTGCAAAGGCCGGAT-3' 3'
3' 3'-CTAGTTCCGCAATGTACT.....AGTCAAACGTTTCCGGCCTA-5' 5'
5'-GATCAAGGCGTTACATGA-3'
Primer
219 base pairs
Sequence-tagged site
(Resolution 1 base)

These maps include the overlap relationships between cosmid contigs and YACs, the regional localization of contigs, YACs, and STSs, and the integration of the genetic-linkage map with the physical contig map.

Figure 12 illustrates the levels of resolution at which information about chromosome 16 is available and also illustrates how STSs serve to integrate the various types of information and levels of resolution. These mapping data, in combination with the resources used to generate the data (the high-density arrays of cosmid clones, the pooled YAC library, the STSs, and the hybrid-cell panel), are already proving useful for the isolation of disease genes and other important regions on chromosome 16. For example, these resources were used to complete the map for the metallothionein gene family, to isolate the chromosome 16 microdeletion region associated with Rubenstein-Taybi syndrome, and to identify chromosome 16-specific repetitive DNA sequences associated with rearrangements of this chromosome that accompany a type of acute nonlymphocytic leukemia.

Several national and international collaborative efforts (described in the accompanying box) are now underway to isolate a variety of disease genes on chromosome 16. Each of these efforts takes advantage of the physical mapping progress on chromosome 16, and collectively they illustrate how the physical mapping of the human genome already has far-reaching significance in the field of medicine.

Completing the Map and Looking toward the Future

In line with the mapping goals stated in the Human Genome Project's Five-Year Plan, the completed map of chromosome 16 will have at most 100 contigs with lengths of between 1 and 2 million base pairs. The contigs will be ordered along the chromosome and represent at least 99 percent of the DNA within it. Moreover the map will be dotted with STS markers at intervals of 100,000 to 200,000 base pairs. Every region of the chromosome will then be rapidly accessible by STS screening of a genomic YAC library.

To complete this final map, we will be making a second YAC library of chromosome 16 by using a restriction enzyme whose restriction sites have a distribution pattern different from those of *Cla*1 (which was the restriction enzyme used in the construction of the first YAC library). A directed approach will then be used to screen this library (and a total genomic library if necessary) for YACs that extend the current YAC-cosmid contigs. We expect that most of the remaining gaps can be closed in this manner. The ongoing development of STSs from the original 576 cosmid contigs will provide the framework for an STS map at a resolution between 100,000 and 200,000 base pairs.

The approach we used to map chromosome 16 is resulting in a high-resolution map of this chromosome. The repetitive-sequence fingerprinting of cosmid clones, the subsequent assembly of contigs, and the evaluation of contig accuracy and chromosome coverage through hybridization experiments have produced a robust map with information on sizes, ordering, and sequence complexity of DNA restriction fragments. Mapping data of this type are invaluable for interrelating chromosome structure with function. Already the chromosomal distribution of $(GT)_n$ repeats has been determined from those data.

With the advent of YAC and PCR technologies, it is now possible to rapidly produce a lower-resolution map of an entire chromosome. YAC clones are 10 to 20 times larger than cosmid clones, so far fewer are needed to create a complete contig map. The assembly of contigs by STS-content mapping is relatively efficient and straightforward. Although physical maps constructed from YAC clones and STS markers will not be as useful for elucidating the structure-function relationships of chromosomes as those made from cosmid clones, the YAC maps still permit immediate access to genes or regions of medical and scientific importance. Consequently, in developing a strategy to map a second chromosome, chromosome 5, we chose to exploit the new technologies. Deborah Grady at our Laboratory and John Wasmuth at the University of California, Irvine, have begun a collaborative effort using chromosome-specific STSs and YAC libraries to rapidly generate a relatively low-resolution map of chromosome 5. Their strategy and some early data are presented in "Mapping Chromosome 5." ■

Collaborations on the Isolation of Disease Genes on Chromosome 16

Polycystic Kidney Disease (PKD1). Polycystic kidney disease is a common dominant single-gene disorder (affecting at least 1 in 1000 Caucasians) that is responsible for cystic kidneys, accompanied by hypertension and renal failure. The principal locus for the genetic defect, PKD1, has been assigned to chromosome band 16p13.3 by genetic linkage with polymorphic DNA markers shown to reside in that band.

Steve Reeders (Yale University School of Medicine), Anna-Maria Frischauf (Imperial Cancer Research Fund), and collaborators have constructed both a long-range restriction map (covering 1 million base pairs) and an ordered contig map (covering 75,000 base pairs) that span the entire PKD1 region. Construction of the contig map by cosmid walking from multiple start sites within the region was greatly aided by the use of two chromosome 16-specific cosmid libraries constructed at Los Alamos. A gene-by-gene search is now being carried out in the region to identify candidate disease genes (genes that are expressed in the kidney and that have alleles that are specific to affected individuals). This effort will probably soon lead to the identification of the gene that is responsible for the disease.

Batten's Disease (CLN3). Batten's disease is a juvenile-onset neurodegenerative disease with incidence rates of up to 1 in 25,000 live births. It is characterized by the accumulation of autofluorescent fatty pigments in neurons. The responsible locus (CLN3) is inherited in an autosomal recessive pattern. That is, the defective allele must be present on both chromosomes in order for the disease to be manifested. The gene responsible for this disease has been mapped to the region between two polymorphic markers in the chromosomal band 16p12.

We have found thirteen cosmid contigs and one YAC clone from our physical map that lie in this same interval, and in collaboration with groups in London (Mark Gardiner), the Netherlands (Martijn Breuning), and Australia (David Callen), we are developing new polymorphic DNA markers from these contigs in an attempt to find markers that are closer to the disease locus. We have used prior knowledge of the repetitive-sequence fingerprint of four of these cosmid clones to develop STSs containing GT-repeat sequences present on these clones. Since GT repeats tend to be variable in length, we expect these STSs to be polymorphic and therefore useful for linkage analysis. We are now evaluating their informativeness in linkage studies. (Genetic-linkage markers for the remaining cosmids are being developed by the other laboratories with the aid of the fingerprint data.) The development of these new genetic-linkage markers in the Batten's-disease region will allow the disease gene to be localized to a manageable region (approximately 1 million bases). Then construction of a detailed physical map starting from the existing contigs and YACs in the region can be completed. The availability of the Los Alamos clones in the Batten's region has substantially reduced the extensive work that would have been required to find genetic-linkage markers from this region and to construct a complete map of the region.

Familial Mediterranean Fever (FMF). FMF is an autosomal recessive form of arthritis that is characterized by acute attacks of fever with inflammation of the lining of the abdominal cavity (peritonitis), pleural cavity (pleurisy), and joints (synovia). The gene frequency among non-Ashkenazic Jews, Armenians, Turks, and Middle Eastern Arabs is comparable to the gene frequency for cystic-fibrosis defects among Caucasians (1 in 25). As with Batten's disease, genetic-linkage markers flanking

the disease locus have been identified by researchers led by Dan Kastner at the National Institutes of Health. We are working with that group to identify contigs and YACs that lie within this region so that additional genetic-linkage markers can be developed.

Rubenstein-Taybi Syndrome (RTS). RTS is characterized by abnormal facial features, broad thumbs and big toes, and mental retardation. RTS is a rare disorder that accounts for an estimated 1 in 500 institutionalized cases of mental retardation. Almost all cases seem to arise from spontaneous mutations. Three patients with RTS have been found to have translocations involving the short arm of chromosome 16. Using fluorescence in-situ hybridization, Martijn Breuning (Leiden University) was able to pinpoint the location of breakpoints in two of these patients relative to cosmids that he had ordered in the region in his group's effort to map breakpoints associated with ANLL M4. One of these cosmids, RT1, appeared to be very close to the breakpoints and was found to be deleted in 6 out of 24 patients. By screening our gridded arrays of chromosome 16 cosmids with RT1, Breuning identified one cosmid, 316H7, that overlapped RT1 by 10 kilobases. This overlapping cosmid was also hybridized to metaphase chromosomes from the two patients with RTS. In both cases, Breuning found three signals, one on the normal chromosome 16, a second signal on the aberrant chromosome 16, and a third on the chromosome that the p arm of 16 had translocated to. These results indicated that cosmid 316H7 spanned both translocation breakpoints in these RTS patients. Since the gene(s) responsible for RTS is likely to be disrupted by these breakpoints, the identification of cosmid 316H7, which spans the breakpoints, opens the door for identification of the gene(s) that causes this syndrome.

Acute Nonlymphocytic Leukemia (ANLL). In contrast to PKD1, CLN3, and FMF, which follow a Mendelian pattern of inheritance, acute nonlymphocytic leukemia is a polygenic trait, that is, it involves the interaction of several genes. A high frequency of rearrangements (inversions and translocations involving both the p and q arms) of chromosome 16 is associated with a specific subtype of acute nonlymphocytic leukemia known as ANLL subtype M4 (see "What's Different about Chromosome 16?"). This association suggests that chromosome 16 may contain at least one of the genes involved in the progression of the disease state and that the chromosomal rearrangements disrupt the functioning of that gene. We are collaborating with groups in the United States, Australia, and the Netherlands to isolate the chromosomal breakpoint regions associated with ANLL. Our prior identification of chromosome 16-specific repeats that map near these regions is aiding the search for the breakpoint regions. Genes that are disrupted as a result of the chromosomal rearrangements will be candidates for having a role in ANLL.

Breast Cancer. Like ANLL, breast cancer appears to be a polygenic trait involving specific alterations of chromosome 16 in addition to alterations in other genes. Deletions in the q22 region of chromosome 16 that are not always detectable at the gross microscopic level occur at a relatively high frequency in the malignant cells of breast tumors. These deletions are readily detectable using fluorescence in-situ hybridization by noting the absence of a positive hybridization signal from a probe that usually hybridizes to the deleted region and the presence of a signal from a second probe that hybridizes to the centromere. We have sent cosmid clones from the q arm of chromosome 16 to Joe Gray (UCSF), who is attempting to pinpoint the region of deletion associated with breast cancers. A gene-by-gene search through the deleted region will presumably lead to the identification of a gene whose function suppresses the development of cancer (tumor-suppressor gene). ■

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WHAT'S DIFFERENT ABOUT CHROMOSOME 16?

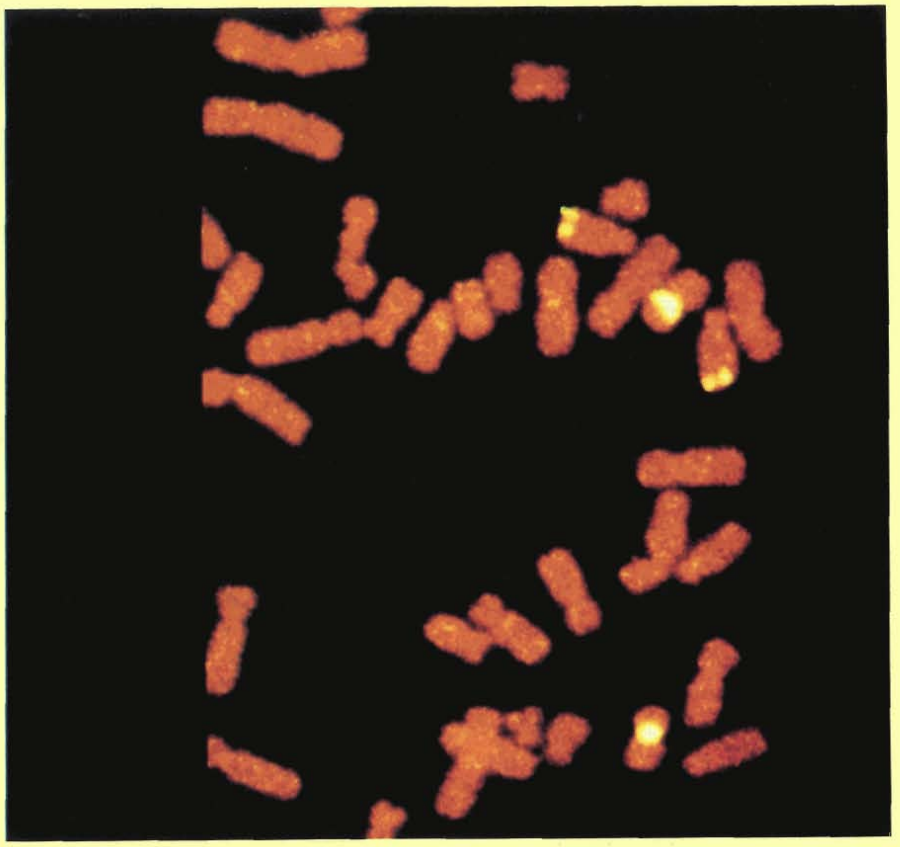
Raymond L. Stallings and Norman A. Doggett

Human chromosome 16 is different from most other human chromosomes in that it contains a larger-than-average fraction of repetitive sequences. As we will describe below, during the course of constructing a contig map for chromosome 16, we discovered several new low-abundance repetitive sequences that are present only on chromosome 16 and that may be implicated in the etiology of certain genetic diseases.

Repetitive sequences are frequently referred to as junk DNA because it has been difficult to determine whether these sequences have any role in the organization and functioning of eukaryotic genomes. Repetitive sequences are also referred to as selfish DNA because they represent such a large fraction of these genomes. For example, the fraction of repetitive DNA in the human genome is estimated to be between 25 and 35 percent. The fact that some classes of repetitive sequences, such as the alpha satellite DNA found in primates, have mutated rapidly over evolutionary time scales lends credence to the notion that at least some repetitive sequences represent mere clutter and play no functional role.

In contrast, work led by Bob Moyzis here at the Laboratory has shown that the repeat sequences that make up the functional centromeres and telomeres of human chromosomes have been highly conserved throughout evolution and serve very important functions. The centromeric repeat sequences are essential to the proper replication and parceling out of chromosomes to daughter cells during cell division. The telomeric tandem repeats maintain the ends of the chromosomes during replication. Some simple microsatellite repeat sequences, such as $(GT)_n$, are so widely distributed throughout all eukaryotic genomes that it is difficult to believe they don't have some functional significance. (See "Various Classes of Human Repetitive DNA Sequences.")

Regardless of whether different classes of repetitive sequences have specific functions or, as Orgel and Crick suggest, are "the ultimate parasite," many of these sequences are of medical interest. Recent findings demonstrate that some human repetitive sequences undergo rapid mutations or facilitate chromosomal rearrangements and that both types of changes can lead to human genetic diseases. The fragile site on the human X chromosome is an example. Like other fragile sites, the fragile X site is so named because the X chromosome at that site appears to have a non-staining gap or break under certain experimental conditions. The fragile X site is located on the X chromosome within the region Xq27.3. Fragile X is inherited in a Mendelian fashion. Recent cloning of the fragile X region and subsequent analysis showed, first, that it contains the trinucleotide tandem repeat sequence $(CCG)_n$, and second, that the tandem repeat can undergo significant amplification (that is, n can increase significantly) between one generation and the next. Moreover, amplification of $(CCG)_n$ seems to be the cause of a very common form of mental retardation that has long been associated with the presence of the fragile X site.



Photograph courtesy of David Ward, Yale University School of Medicine

Shortly after the dramatic discovery of the fragile X site came reports that amplification of another trinucleotide repeat on chromosome X, $(CTG)_n$, is responsible for spinal and bulbar muscular atrophy and that amplification of the $(CTG)_n$ repeat on chromosome 19 is responsible for myotonic dystrophy. Evidently, when those tandem repeats undergo spontaneous amplification within germ-line cells, they disrupt the functioning of a gene or of the regulatory region for a gene in an offspring derived from a gamete containing the amplified sequence. The increasing level of amplification from one generation to the next is accompanied by an increase in the symptoms of the disease, a genetic process that has been termed anticipation. For example, amplification of $(CTG)_n$ that occurs in one generation may cause cataracts, and its further amplification in a subsequent generation will cause full-blown myotonic dystrophy.

Repetitive sequences other than trinucleotide tandem repeats have also been implicated in genetic disease. For example, it was recently discovered that the insertion of a truncated L1 sequence in the gene for blood-clotting factor VIII was responsible for a spontaneous case of hemophilia A. Similarly, de novo insertion of Alu repeats into the cholinesterase gene led to inactivation of the gene, and a comparable insertion in the NF1 gene caused the common dominant disorder known as neurofibromatosis type 1.

Our group and a group at Leiden University have recently determined that there is extensive sequence homology between two widely separated regions of chromosome 16, band 16p13 on its short arm and band 16q22 on its long arm. The homology could explain why rearrangements occur between those chromosomal regions in acute nonlymphocytic leukemia (ANLL). The sequence homology between the two bands is due to the presence of low-abundance repetitive sequences at multiple loci in bands 16p13, 16p12, 16p11, and 16q22.

We discovered those repetitive sequences on chromosome 16 in the course of developing the contig map of chromosome 16. As we grouped pairs of overlapping clones into contigs, we encountered an anomaly—a set of 78 clones, all of which seemed to overlap other clones in the set. Thus the clones appeared to form a single contig, or island of overlapping clones, much larger than the average contig, which contained only four or five clones. However, when we tried to position the clones to form a

single contig, we found that they could not be placed in a linear order, but rather the contig branched in many directions and included many clones that seemed to be piled on top of one another. Our inability to construct a linear contig indicated that many false overlaps had been deduced from the fingerprint data because of the presence of some unknown repetitive sequence in the clones.

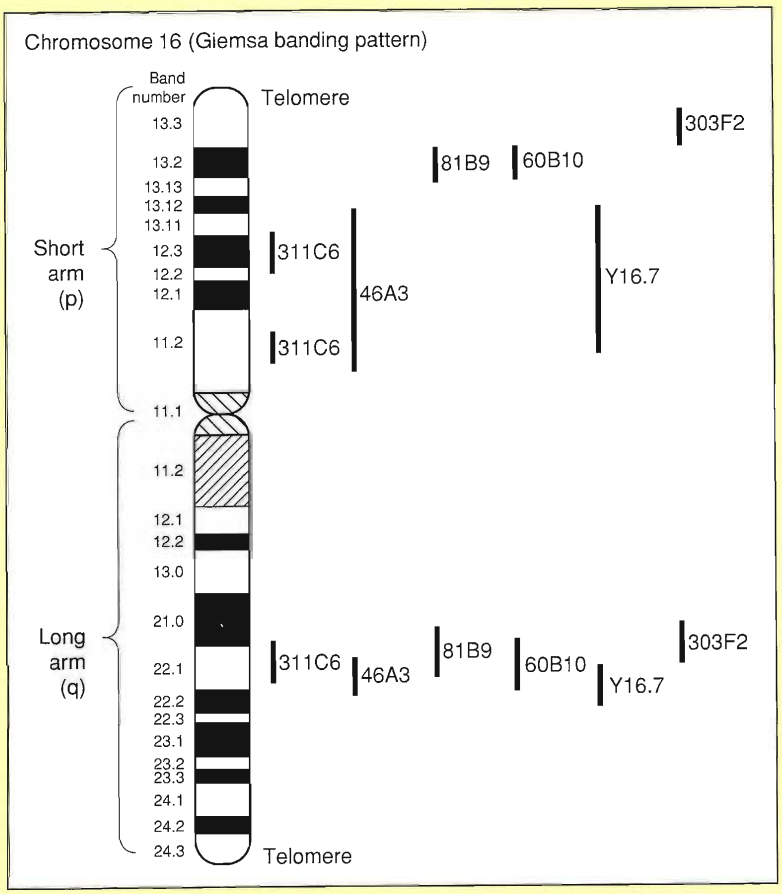
We went on to analyze the 78 clones using a variety of techniques. Fluorescence in-situ hybridization of five of the clones revealed that each one hybridized to as many as three locations on chromosome 16, and those locations occurred in four bands of chromosome 16: 16p13, 16p12, 16p11, and 16q22 (see Figure 1). The hybridization results and further analysis indicated that the four bands contain low-abundance repetitive sequences that are found only on chromosome 16. Characterization of one of those sequences revealed that it was a minisatellite-type sequence that did not possess homology to any of the known minisatellites. The consensus repeat unit of the sequence is

TCCT X TCCT CTTCCACCCT CAGTGGATGA TAATCTGAAG GA,

where X is any sequence containing between 2 and 9 nucleotides. The results of in-situ hybridization of this consensus repeat to chromosome 16 is shown in the opening pages of "The Mapping of Chromosome 16." High-stringency hybridization of the consensus sequence to Southern blots containing DNA from humans, the rhesus monkey, rat, mouse, dog, cow, rabbit, chicken, and yeast produced positive hybridization signals only from human and monkey DNA. Apparently, the sequence is present only in primates and therefore could be relatively recent in origin.

We estimate that the low-abundance repetitive sequences specific to chromosome 16 together occupy between 2 million and 6 million base pairs of the chromosome. Moreover, those sequences appear to overlap the breakpoint regions involved in the rearrangements of chromosome 16 commonly observed to accompany the particular subtype of acute nonlymphocytic leukemia referred to as ANLL subtype M4. Those chromosomal rearrangements include an inversion around the centromere between breakpoints in bands 16p13 and 16q22, a translocation between the homologs of chromosome 16 involving bands 16p13 and 16q22, and deletions in 16q22. Recombination between the low-abundance repetitive sequences in bands 16p13 and 16q22 could lead to the observed inversions and translocations. Therefore it is not unreasonable to consider that the repetitive sequences may be causally related to the inversions and translocations that occur in the chromosomes of leukemia cells. The isolation of repetitive sequences common to bands 16p13 and 16q22 is facilitating the isolation of the breakpoint regions and any gene(s) that may reside at those breakpoints.

We have discovered not only low-abundance repetitive sequences in the euchromatic arms of chromosome 16 but also novel repetitive sequences at the pericentromeric regions (regions near the centromere) of human chromosome 16 and at locations on other human chromosomes. The latter repetitive sequences are distinct from



any of the five satellite sequences (α, β, I, II, III) that are commonly found in the centromeric region of all human chromosomes. Previous work at the Laboratory had revealed that a large block of chromosome-specific, satellite-II-variant DNA occurs at the pericentromeric region of the long arm of chromosome 16 (at 16q11.1) and that a chromosome-specific α-satellite variant occurs in the centromeric region of chromosome 16. We have identified a new repetitive sequence that appears as a large block on the pericentromeric region of the short arm of chromosome 16 (at 16p11.1) and is also found in the telomeric regions of chromosome 14 (Figure 2). This block of repetitive sequence at 16p11.1 composes almost 2 percent (or 2 million base pairs) of chromosome 16. In addition, we have found another repetitive sequence that maps to 16p11.1 and 15q11.1.

The region 16p11.1 appears to be quite rich in novel repetitive DNA sequences that map to a few other human chromosomes. Another minisatellite, MS29, maps to 16p11.1 and to chromosome 6. The MS29 locus at 16p11.1 is polymorphic in that it is absent from some human chromosomes 16. Several other unusual chromosome-16 variants have also been reported that appear to have extra material added in band 16p11.1 The extra material is C-band negative; that is, it does not darken when stained by the special techniques that usually darken only the centromeric regions. Also, the extra material is not composed of α-satellite DNA.

With the extensive amount of repetitive DNA found at 16p11.1, one might expect to find occasional amplification of this region. The amplification of this DNA does not appear to have any phenotypic effect, although the possibility of increased risk of aneuploidy cannot be ruled out. Also, the possibility that further amplification in successive generations could have detrimental effects cannot be ruled out. ■

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Mapping Chromosome 5 *Deborah Grady*

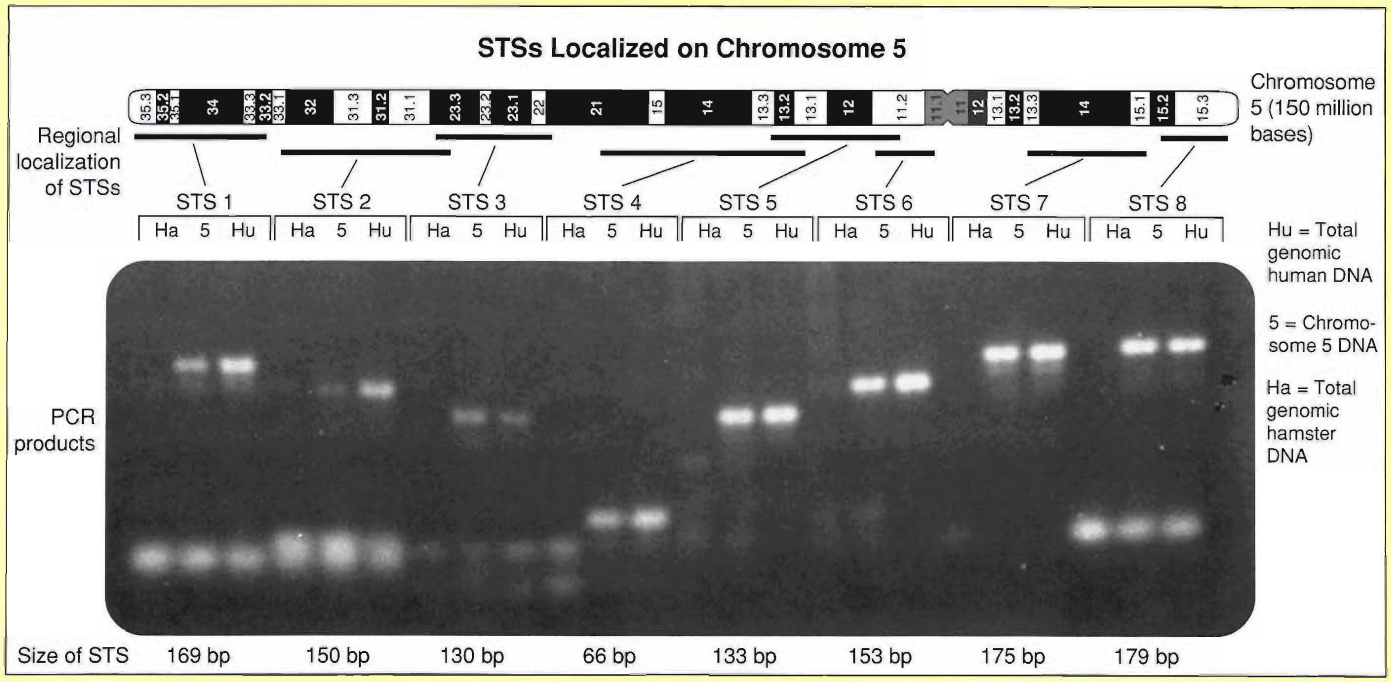
Constructing physical maps of complex genomes relies on the ability to isolate DNA segments for detailed analysis and to position those segments along the genome by identifying physical landmarks within them. The chromosome-16 physical map, now nearing completion, is a high-resolution map of DNA segments that have been isolated through cloning in cosmid and YAC vectors. The cloned fragments have been assembled into contigs and positioned along the chromosome based on detailed information about the positions of restriction sites, repetitive sequences, and the unique physical landmarks called STSs, or sequence-tagged sites. The chromosome-16 contig map provides information at a resolution of about 10,000 base pairs and will prove useful in studying chromosomal structure and organization.

In view of the need to complete physical maps of other chromosomes both rapidly and efficiently, we are adopting a different approach in mapping a second chromosome, chromosome 5. The goal is to construct a lower-resolution map consisting of (1) a series of STSs spaced evenly across the chromosome; and (2) YAC contigs assembled and ordered along the chromosome on the basis of their STS content. The project is being carried out in collaboration with John Wasmuth of the University of California at Irvine.

Our starting strategy utilizes the Los Alamos technologies for constructing chromosome-specific libraries to rapidly build a map covering 60 percent of the chromosome. The first step is to create a "framework" map of STS markers spaced at intervals of 0.5 to 1 million bases along chromosome 5. Given the statistics associated with generating STS markers at random and the fact that chromosome 5 is 194 million bases long, we will have to generate at least 400 STS markers to produce an STS map with a resolution of 1 million base pairs. We are developing the STS markers from a chromosome 5-specific library of M13 clones constructed at Los Alamos specifically for this purpose. Generating an STS involves sequencing a short cloned fragment of genomic DNA and identifying unique primer pairs from that sequence, which, when used in the polymerase chain reaction (PCR), will amplify a unique site in the genome. (See "The Polymerase Chain Reaction and Sequence-tagged Sites.")

Wasmuth is localizing the position of each STS to one of the intervals along human chromosome 5 defined by a panel of 30 hamster/human hybrid cells each containing various portions of chromosome 5. This localization is accomplished by determining through PCR screening which hybrid cells contain the STS and which do not. This method allows regional localization at a resolution of between 5 and 10 million base pairs. Plans are being made to refine the localization to a resolution of 200,000 base pairs using radiation-hybrid mapping. This mapping technique is analogous to genetic-linkage mapping in that distances are measured by how often two markers on the same chromosome become separated from one another. In linkage studies the separation is due to crossing over during meiosis, and the frequency of crossing over, the so-called genetic distance, is not necessarily proportional to the physical distance. In radiation-hybrid mapping the separation occurs through radiation-induced chromosome breakage, and the frequency of the radiation-induced breakage between two markers is linearly proportional to the physical distance separating the markers. Moreover, the technique is readily applied to any unique markers, in particular, to STSs.

Once generated and regionally localized on the chromosome, each STS will be "anchored," or located, on a non-chimeric YAC clone from a chromosome 5-specific YAC library, which has been constructed at Los Alamos. The cloning technique used to construct non-chimeric clones from flow-sorted chromosomes is discussed in "Libraries from Flow-sorted Chromosomes."



The non-chimeric YACs, localized along chromosome 5 by their STS content, will provide a solid base on which to build YAC contigs covering the chromosome. At Los Alamos, we will concentrate on mapping the short arm of chromosome 5 (52 million base pairs). Special emphasis will be placed on the region of chromosome 5 involved in the Cri du chat syndrome, one of the most common terminal-deletion syndromes in humans.

The figure (above) illustrates our early work on STS generation and regional localization. The upper portion shows the regional localization along chromosome 5 of eight STSs generated from our chromosome 5-specific M13 library. The regional localization (indicated with bars) will be reduced to intervals of 5 to 10 million bases once all available hybrid cells are screened for the presence of each STS.

The photograph in the lower portion of the figure shows the results of testing for the existence and uniqueness of each STS. The three gel lanes for each STS show the PCR products generated from total-genomic human DNA (right lane), chromosome-5 DNA (middle lane), and total-genomic hamster DNA (left lane) using the primer pairs that operationally define each STS. The PCR products from the three reactions were separated in parallel in a 3 percent agarose gel and stained with ethidium bromide to visualize the DNA. In all cases a single PCR amplification product of the same size resulted from the total-genomic human DNA and the chromosome-5 DNA. The hamster DNA served as a control to ensure that a positive signal from the chromosome-5 DNA did not represent a spurious signal arising from hamster DNA. In all cases, the hamster DNA yielded no PCR product. The test also shows that human/hamster hybrid cells can be screened for an STS without concern that false positive signals will arise from the hamster DNA in the hybrid cell. The PCR results demonstrate the existence of each STS as a unique landmark on chromosome 5 and the specificity of the PCR protocol defining each STS. The size of each STS is given at the bottom of the figure. ■